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OM protein - protein search, using sw model

Run on: January 24, 2003, 19:40:10 ; Search time 35 Seconds
(without alignments)
2095.794 Million cell updates/sec

Title: US-09-675-509-4

Perfect score: 1802

Sequence: 1 MSQPKTLVGLFPLPSMN.....CVDPAKENVKAGVLRPFL 356

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

T number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	118.5	6.6	345	16	Q8RD78
2	116	6.4	1248	10	Q9SAJ2
3	115	6.4	286	2	Q9RLV6
4	114.5	6.4	1431	5	Q9XYH6
5	112.5	6.2	1360	5	015807
6	111.5	6.2	613	17	Q97YF0
7	111.5	6.2	1414	17	Q8TH79
8	111	6.2	417	16	Q8RBL7
9	110.5	6.1	912	11	Q94JF5
10	110.5	6.0	448	10	024399
11	109	6.0	998	5	044800
12	108.5	6.0	528	5	Q20730
13	108	5.9	2081	17	Q9HU37
14	107	5.9	1007	9	Q9FAJ3
15	106.5	5.9	1033	10	Q9CAA7
16	106.5	5.9			

17	106.5	5.9	1166	12	Q8V7X1	Q8V7X1 chlorella v
18	106.5	5.9	2819	16	Q980P8	Q980P8 mycoplasma
19	106	5.9	545	17	Q9Y283	Q9Y283 pyrococcus
20	106	5.9	1054	16	Q9PR50	Q9PR50 ureaplasma
21	106	5.9	1220	3	Q9P3A8	Q9P3A8 schizosach
22	105.5	5.9	358	16	Q928M1	Q928M1 listeria in
23	105.5	5.9	602	16	Q8RBX6	Q8RBX6 thermoaer
24	105.5	5.9	1277	16	Q50698	Q50698 borrelia bu
25	105	5.8	1058	13	Q91943	Q91943 carassius a
26	104.5	5.8	503	17	Q97XR3	Q97XR3 sulfolobus
27	104.5	5.8	628	16	Q9PQ47	Q9PQ47 ureaplasma
28	104.5	5.8	2462	16	Q8RGZ3	Q8RGZ3 fusobacteri
29	104.5	5.8	2806	16	Q8RI19	Q8RI19 pseudomonas
30	104	5.8	689	2	Q8RSZ0	Q8RSZ0 sulfolobus
31	103.5	5.7	692	17	Q97YM6	Q97YM6 methanobac
32	103.5	5.7	1733	17	Q8TTS9	Q8TTS9 drosophila
33	103.5	5.7	4643	5	Q9VW71	Q9VW71 drosophila
34	103	5.7	286	16	Q9CIN5	Q9CIN5 lactococcus
35	103	5.7	637	16	Q9ZDM5	Q9ZDM5 listeria in
36	103	5.7	738	2	Q9AQF4	Q9AQF4 clostridium
37	103	5.7	1857	3	Q8TSC5	Q8TSC5 aspergillus
38	103	5.7	2701	6	Q8W96	Q8W96 bos taurus
39	102.5	5.7	598	2	Q9L746	Q9L746 haemophilus
40	102.5	5.7	704	16	Q31399	Q31399 bacillus su
41	102	5.7	578	10	Q9SDM7	Q9SDM7 glycine max
42	101.5	5.6	505	5	Q93335	Q93335 caenorhabdi
43	101.5	5.6	703	16	Q93MA0	Q93MA0 clostridium
44	101.5	5.6	728	10	Q9W9S4	Q9W9S4 arabidopsis
45	101.5	5.6	767	5	Q94543	Q94543 drosophila

ALIGNMENTS

RESULT 1

Q8RD78 PRELIMINARY; PRT; 345 AA.

ID Q8RD78

AC Q8RD78; 01-JUN-2002 (TEMBLrel. 21, Created)

DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)

DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)

DE Sporulation protein and related proteins.

GN SPOLID OR TBE0168.

OS Thermobacter tengcongensis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;

OC Thermobacteriaceae; Thermobacteriaceae; Thermobacter.

OX NCBI_TaxID=119072;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MB4T / JCM11007;

RX MEDLINE=21992816; PubMed=11997336;

RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

RA Tan H., Chen R., Wang J., Yu J., Yang H.;

RT "A complete sequence of T. tengcongensis genome.";

RL Genome Res. 12:689-700(2002).

DR EMBL; A012990; AAM23469.1; .

KW Complete proteome.

SQ SEQUENCE 345 AA; 38528 MW; B75DD6A0FB99AC57 CRC64;

Query Match 6.6%; Score 118.5; DB 16; Length 345;

Best local similarity 21.3%; Pred. No. 3;

Matches 73; Conservative 60; Mismatches 118; Indels 91; Gaps 17;

QY 21 ENGSEVKILINIK-DVLEPTQVSGYN-IEYTEFDCYSDASLOS-LPDVFSTDSI----- 70

Db 41 EGGKSVKDKLPSYEVIRVFPTNQNKIEEMQLEIDYVGVVAEMPAEFELALKAQAVAA 100

QY 71 ---FLPVIYSVGKVSUDESIVRGVTDLHGFVSASSSVNGSVYGPQYLCSNFLSSPN 127

Db 101 RTYLAKEVALG-----KGC--DLHEGVD-----VCTD-----PE 129

QY 128 GTQASSLLEIAKVG-----YEQI-----VYPDVASSSFTVGLYQQLQ 169

Db 130 HQAQSIBELKKGKNGENFEKYKISQAVDSTKGLVMVYQDA-----LIPVTHAISG 183
Qy 170 SSSSAVDIKASDLPQSGDQVN--KDITOKYRTILDSTVVASQREYINSVKQKPISNYY 227
Db 184 GRTESEEDVMQKIKIPLYKSVSPGEEVASKYKT-----FTVVSQAEPVKKLKERQF--SLK 237
Qy 228 VQSSSMCEIKIITIDQOYNVOLIGTSDKPY--VYTDVLALNS--NLCEKQKVAVEYIK 283
Db 238 LTSNNILBEIKIERTQAGHVTKLIGDVFEGKEIKELFGINSNFTFSKQK----- 290
Qy 284 NLTLTIVLDLGLTLTPANKNGIAHLAKSSNPFYAOLSOQF 325
Db 291 ----DDIVITVIGYGHGVMGQYGANALAKEGKFDILIKY 328

RESULT 2

Q9SAU2 PRELIMINARY; PRT; 1248 AA.

01-MAY-2000 (Tremblrel. 13, Created)
01-MAY-2000 (Tremblrel. 13, Last sequence update)
01-MAR-2002 (Tremblrel. 20, Last annotation update)
T8K14.1 protein.
T8K14.1.
GN Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV_COLUMBIA;
RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
RA Li J., Kremenetskaia I., Lueros J., Lee J.M., Gonzalez A., Altat H.,
RA Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
RA Huizar L., Kim C., Palm C., Rowley D., Shin P., Walker M.,
RA Davis R.W., Ecker J.R., Federpiel N.A., Theologis A.;
RT "Arabidopsis thaliana chromosome 1 BAC T8K14 sequence."
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC007202; AAD30219.1; -.
DR HSSP; P08631; IAD5.
DR InterPro; IPR000719; Euk_Pkinase.
DR InterPro; IPR004040; STY_Pkinase.
DR InterPro; IPR001245; Tyr_Pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Euk_Pkinase; 1.
F SMART; SMO0221; STYK; 1.
F PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
KM ATP-binding; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 1248 AA; 137242 MW; 0EE4A8B99C50328 CRC64;

Query Match 6.4%; Score 116; DB 10; Length 1248;

Best Local Similarity 19.1%; Pred. No. 27;
Matches 75; Conservative 69; Mismatches 123; Indels 126; Gaps 17;

Qy 14 FYLPSW-----NENGNEVKLN-----LIKD-VLPTQVS----- 41
Db 26 PFMPOQTGSASANMRPNSNGSDVKAHNFISIQTEEFSLFERMRDVIIPQRSSNPNGACD 85
Qy 42 -GVNIEYEF-----DCVSDASIQS-----LDVFTDLSIFLPYVLSGCVSL 84
Db 86 MMYNTGVELKGLIGISHTGSECADVSRFSTVENGTSDIERTNSLHEFGKLNHVQSA 145
Qy 85 DESLVR--GVTGDLHSFVSSASVNGSVYGFPOYLCS--NFLSSPNGTQ-----QASL 135
Db 146 FOALLSKSSQGNLHGYNKNTSSASGSAVTAKYLCSFGKILPPRQSKLRYVGGEITHI 205
Qy 136 LELAQVGYEQI-----VYPDVASSSFTVFGLYQ-----QLIQSSSSAAVDIKASD 182
Db 206 ISIRKDISMOELROKILRIY-----YQTRVVKYQLPGEDLDLALVSVSSEED 251

Qy 183 ----LPSGDOVKDITOKYRTILDSTVVASQREYINSVKQKPISNYYGVGSMSCEIK 238
Db 252 LQNNLEEYENENENGGSKQKLMFLFS--ISDMDALLGVNNDSDSEF----- 297
Qy 239 DIIRDOQYNVOLIGSDKPYVYTDVLALNSNLCEKQKVAVEIKNLTNTVLTLGLGL 298
Db 298 -----QTVVAVNGMDIOGSKNSTILGLDSSANNLAELDVNRTEGI--NTIAGDVGVG 349
Qy 299 LTLPAKNGIAHLAKSSNPFYAOLSOQFPDAKES 331
Db 350 -----ASQLMVGFOQTSAQOSE 367

RESULT 3

Q9RLV6 PRELIMINARY; PRT; 286 AA.

01-MAY-2000 (Tremblrel. 13, Created)
01-MAY-2000 (Tremblrel. 13, Last sequence update)
01-JUN-2002 (Tremblrel. 21, Last annotation update)
De Hypothetical 32.0 kDa protein.
OS Lactococcus lactis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1358;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG1363;
RX MEDLINE=20112344; PubMed=10647818;
RA Aungmyapornchai P., Griffin H.G., Gasson M.J.;
RT "Cloning, DNA sequence analysis, and deletion of a gene encoding
RT diacetyl-acetoin reductase from Lactococcus lactis."
RL DNA Seq. 10:163-172 (1999).
DR EMBL; AJ012388; CAB59827.1; -.
DR InterPro; IPR004872; Lipoprotein_9.
DR Pfam; PF03180; Lipoprotein_9; 1.
KM Hypothetical protein.
SQ SEQUENCE 286 AA; 31960 MW; 4B4A81A83D34314B CRC64;

Query Match 6.4%; Score 115; DB 2; Length 286;

Best Local Similarity 22.2%; Pred. No. 3.9;
Matches 47; Conservative 42; Mismatches 85; Indels 38; Gaps 7;

Qy 13 FPLYPSWNE--NENGNEVKLNIKVLPQVSGNYIEFTPCYDASIQSLPDPFSTDSI 70
Db 99 YAYLKSNNKANNNGNIVS---IGDTITTPHLVSTKYKVDLPDKSTIALPNDITNESR 154
Qy 71 FLPLVLSGCVKSDSESLVRGVTGDLHSFVSSASVNGSVYGFPOYLCSNFLSSPNGTQ 130
Db 155 AL-YVLKNAAGLIKIDTS--KGLATVADIRENPKSL-----IIEIDASQ 196
Qy 131 QASLLELAQVGYEQIYVDPVASSSFTVFGLYQQLIQSSSSAAVDIKASDLPQSGDQV 190
Db 197 TPRALDSVAAV---INYNFAISAKNSDKESIYQEPINEDSAQWINFIAHQDKNNKV 252
Qy 191 NKDITOKYRTILDSTVVASQREYINSVKQKPY 222
Db 253 YKEVAVKAY-----EOKNIADIITKEYP 274

RESULT 4

Q9XYH6 PRELIMINARY; PRT; 1431 AA.

01-NOV-1999 (Tremblrel. 12, Created)
01-NOV-1999 (Tremblrel. 12, Last sequence update)
01-JUN-2002 (Tremblrel. 21, Last annotation update)
De ATP-binding cassette protein.
GN CPABC.
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.

Query Match	6.4%;	Score 114.5;	DB 5;	Length 1431;
Best Local Similarity	22.9%;	Pred. No. 42;		
Matches 89;	Conservative 61;	Mismatches 142;	Indels 97;	Gaps 21;

RESULT 5	
015807	
ID 015807	PRELIMINARY;
015807	PRT; 1360 AA

DT 01-JAN-1998 (TrEMBLrel.05, Created)
 DT 01-MAR-2002 (TrEMBLrel.20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel.21, Last annotation update)
 DE ATP-binding cassette protein 1 (Fragment).
 GN ABC1.
 OS Cyctosporidium parvum.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida
 CC Cyctosporididae; Cyctosporidium.
 NX NCBI_TaxID=5807;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KST-1;
 EX MEDLINE=97376910; Pubmed=92333681;

Query Match	6.2%	Score 112.5;	DB 5;	Length 1360;
Best Local Similarity	22.9%	Pred. No. 53;		
Matches 89; Conservative	61;	Mismatches 142;	Indels 97;	Gaps 21.

RESULT 6
Q97YF0
ID Q97YF0
PRELIMINARY;
PRT; 613 AA.

DT 01-OCT-2001 (TEMBLRef1. 18, Created)
 DT 01-OCT-2001 (TEMBLRef1. 18, Last sequence update)
 DT 01-OCT-2001 (TEMBLRef1. 18, Last annotation update)
 DE Hypothesized protein SSO1375.
 GN SSO1375.
 OS *Sulfolobus solfataricus*.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC *Sulfolobus*.

OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Aveyer M.J., Chan-Weher C.C.Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erasus G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Noc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Regan M.A., Sensen C.W., Van der Oost J.,
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2,"
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; A606751; AAK1609.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 613 AA; 67767 MW; F478640AC69BA3 CRC64;

Query Match 6.2%; Score 111.5; DB 17; Length 613;
Best Local Similarity 19.5%; Pred. No. 20;
Matches 85; Conservative 72; Mismatches 113; Indels 165; Gaps 22;

QY 13 FPY---LPSMNGN-----NEVKLIN-IKDVLPTOVSGY-----44
DB 88 YPINOVWNYPENGLPLMNSYDNMSIHESIFALPTVDVYPTKI--YNSSLYLKGLLS 145
QY 45 -----LEYTFDCYSDASLQSLPD--VFSTDSIFLPLYSLGCV-----KSLDES 87
DB 146 ATYKNIATIIISYKDFSKY--NITLSQYPSHILQGTGIGL-FIIPLOQLPMWYKSNVSS 203
QY 88 LVR-----GVTDLHSPVSSASVN-GSYVGFPOYICSNFL 122
DB 204 VIQTYIFQNETNLLINGNDPESLTQGLYDELSTVQTLFELNTSPY-----SSIL 256
QY 123 LSSPFGTOA-----SSLLELA-----OKVGEQIV-----148
DB 257 IDSINNTLEAMNRTTNOTIDNSITDLAYSSSTLTPEGEFFAYIVSPGNTITTKIES 316
QY 149 -----YPDVASSSSFTFGIYQOQLQSSSSAAVDIKASDLPQSGDQVNDKI 194
DB 317 EYISLPKLVMLIQYPSISNQSPTTIVSFVFNLRNSATKREGVVGLIYNSG-----369
QY 195 TQKRTIIDSTVVASQREYINSYKQKPISNY-----VGYSEMEIKDIIRD--QOY 246
DB 370 -----LISKISIMNSNGELVFNVSPTVLYVYHYNLGLNTEYMGQIRIDVRSGINKY 423
QY 247 NVQLIGTSDKPYVTVDVLAUNSLCDEKQKVAVEYIKMLTNTVLDDLGLGLTPANKN 306
DB 424 NF---TVEPVIYIIT---DTSIDQPKISVKIINPL--NOTVSGQLYLWIS-----N 468
QY 307 GIAHLAKSSNFYAOL 321
DB 469 GIASASAPTFESQL 483

RESULT 7
Q8RH79 PRELIMINARY; PRT; 1414 AA.
AC Q8RH79;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein MA4643.
GN MA4643.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Attoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeAtrelino K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.,
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity";
RL Genome Res. 12:532-542(2002).
DR EMBL; AB011187; AAM07977.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1414 AA; 159146 MW; D6F0DECE589A89 CRC64;

Query Match 6.2%; Score 111.5; DB 17; Length 1414;
Best Local Similarity 21.7%; Pred. No. 65;
Matches 83; Conservative 56; Mismatches 148; Indels 95; Gaps 19;

QY 15 YLPSMNGN-----EVKLINIKDVLPTOVSG-----YNIETFDYSDASLQSLPD 63
DB 649 YLTS-KENNNTALMDQYENISIRIKDTHIDEDIGLNFYSNMSYEFE---DTVYGEVH 704
QY 64 VFSTDSIF--LPLYSLGCVKSLDES--LVRYTGDLHSPVSSASVNGSVGFPQYLC 118
DB 705 DYLDHMWYANIPYGLRIFAPRIPISDESAAVALVRGMLGP--SYIEHIQAVNAS-----C 754
QY 119 SNFLSSPNCQOQASL-----LEIAQKVEYEDQIVPDVSSSSFTVFG--LYQOL 167
DB 755 DSHETEEYNKTESYRLLYTVLVDGIDITLQO---BEVLGSSSSAEVEDLVAEYYQNT 810
QY 168 LQSSSSA-----AVDIKASDLPQSGDQVND--ITQKRTIIDSTVVASQREYINSVK 218
DB 811 LLSSESEIKGLDLDAKYIEPSVGDIKSPVLPRGXKPYSDRPLIPKEXV-NIGK 869
QY 219 QGKPISNYVYGVSSMEIKDIIRDQOYNVOLIGTSKPY-----258
DB 870 E--TIDSFIVDYKNEPEPEKVAVLMGIEYMRNHGVPHSQMLYLNGVEPMDANGRV 927
QY 259 VYTVDLAUNSLCDEKQKVAVEYIKMLTNTVLDDLGLGLTPANKNGIAHLAKSSNFY 318
DB 928 YTTPSASNLHIMQSE-LTIRLSNGTVINPRIDVIG-----HSSGLH 970
QY 319 A-QLSQOFDAKSESEVRLRQVD 339
DB 971 RDQFPQMDLLDPAVRILISQLD 992

RESULT 8
Q8RH79 PRELIMINARY; PRT; 417 AA.
AC Q8RH79;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Sugar-binding periplasmic proteins/domains.
GN UGPB OR TTE0799.
OS Thermobacterium tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermobacteriales; Thermobacteriaceae; Thermobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4T / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.,
RT "A complete sequence of T. tengcongensis genome";
RL Genome Res. 12:689-700(2002).
DR EMBL; A6013046; AAM24056.1; -.

KW Complete proteome.
SQ SEQUENCE 417 AA; 46304 MW; C974291CB505202D CRC64;
Query Match 6.2%; Score 111; DB 16; Length 417;
Best Local Similarity 20.8%; Pred. No. 13;
Matches 83; Conservative 68; Mismatches 143; Indels 106; Gaps 19;
QY 2 STOPKTLVGLPFLPSMNGENVEKLTINLIKDVLPQTGSGNIEYTEFD-----51
DB 38 TSKPTITLGM-----WSSSPAEEKIYD-----DGIARFKEKYPRIWDQIETIVGDY 84
QY 52 ---CYSDASLOSLLPVSSTDSIFLPYVLSGVSLSDESLVGVGTDLHSF---VSSSAS 105
DB 85 MQKLQTELASNTAPDIFYLDSEMPAPQLMSSGVLBLEPDE-YIKKYVVDVNDPEPALLSAFQ 143
QY 106 VNGSVYGFPOYLCSNFISSNGTQA-----SSULELAKV---GYEQIYY-PDV 152
DB 144 WEGKTYGLPKDYNLTVLFPYNDMPKEAGINPPKTMWELRETAKKLTNGVKGIVLSADL 203
QY 153 ASSSFTVFGLYQQLSSSAVDIKAS-DLPQSGDQV-----KDTQKXRT 200
DB 204 ARPDFA-----INQDGSVYKDGKVTLLPQNAELDPVGLIIRDKVADTFQNNGE 255
QY 201 ILDSVVASQRE-----YINSYKQKPISNYYVYSGESMCEIKDIIRDOQYVWQLIG 252
DB 256 GMDGDAFAKKAAMIEGGMWIPFLKEKAPDLNY-GIAELPAKCK-----299
QY 253 TSDRPYVTDVLALNSLCEKQKAVAVIKLTLNTLVLDLGLGLPANKGIAHLA 312
DB 300 KSTVAFTVAVMNNKSKKHDEFKL-IEFLTGKEGQGFVVD---SGLALPSRK-----S 349
QY 313 KSNF---YAQLSQGFDAKESEV-----RVLRQVDPFANK 343
DB 350 MEANFKEKYPERRAPRIDASVAVPQFGLYGTKLVDAAANK 389
RESULT 9
QY 094JF5 PRELIMINARY; PRT; 718 AA.
AC 094JF5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE P0684B02.13 protein.
GN P0684B02.13.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eupharitioideae; Oryzaceae; Oryza.
NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0684B02.13";
RU Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003023; BAB44026.1;
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR001807; CI-channel_volt.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00654; voltage_CLC; 1.
SQ SEQUENCE 718 AA; 76362 MW; DAB54F202012785B CRC64;
Query Match 6.1%; Score 110.5; DB 10; Length 718;
Best Local Similarity 26.2%; Pred. No. 29;
Matches 71; Conservative 36; Mismatches 93; Indels 71; Gaps 15;
QY 55 DASIQSLPVDVSTSIPLPYVLSGVSLSDESLVR-GVTGDLHSFVSSASVNGSVYG 112
DB 367 DILLESRP---FTSGLSAAVIVOLIGVYKVLATSLCRAFGLGVGYAPSLFICAAITGMAYG 423
QY 113 PFOYLCNFISSNGTQAASLLELAKVGEQIVYPDVASSSSFTVFGLYQQLSSS 172

DB 424 ---KVMRFPTGPD-----SLF-----OIPFLDVASPOAYGLVGM-----455
QY 173 SAADVIRASDLPOSGDQVNDKITOKYRTILD-----STVVASQREKINVKQKQPISN 225
DB 456 -AATLAGYCKPLTSLVLLFELTQDRIYVLPGLGAVGSWIASPQPSRS-NRSKPDSS 513
QY 226 YVGVSESMCEIKDIIRDOQYV--QLIGTS---DKPYVTDVLALNSLNC--DEKOK-- 276
DB 514 -----EVKSNFQKESVPSQOGASVDIDKP--ITDLCKLSSLCVYDAKHNF 561
QY 277 ---VAEVIK---NLTLNTVLDDLGLGL 299
DB 562 QENTLVAEMAKTKYISVSKTPVVEALNLM 592
RESULT 10
QY 070410 PRELIMINARY; PRT; 912 AA.
ID 070410;
AC 070410;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Putative pheromone receptor V2R2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VOMERONASAL NEURONS;
RX MEDLINE=97436753; Pubmed=9292726;
RA Ryba N.J., Tirindelli R.;
RT "A new multigene family of putative pheromone receptors.",
RN Neuron 19:371-379(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=VOMERONASAL NEURONS;
RA Ryba N.J.P., Tirindelli R.;
RU Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053986; AAC08413.1;
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRNGR.
DR PROSITE; PSS0259; G_PROTEIN_RECP_F3_4; 1.
KM Receptor.
SQ SEQUENCE 912 AA; 102348 MW; 2C54FAB6DBFA48D CRC64;
Query Match 6.1%; Score 110.5; DB 11; Length 912;
Best Local Similarity 21.0%; Pred. No. 41;
Matches 79; Conservative 62; Mismatches 120; Indels 115; Gaps 20;
QY 26 VKLNLKDVLPQTGSGNIEYTEFD-CYS-----DASLSQSL-----PDVFSTDSIFL 72
DB 95 IKETIKRDLIPNHTLTYQI---FDSCYTIISKAMESSLVLTGQEEFKPFRNRSTGSL 150
QY 73 PYVLVSLGVK-SLDESIVRGVGTGDLHSFVSSASVNGSVGFPOYLCSNFISSPNGTQ 131
DB 151 AALVSGSGSSLSVAAKILGLIYVPOYGYTSSCSILSDKQFQPSY-----LRVPSDNLQ 205
QY 132 ASSLLELAKVGEQIVYPDVASSSFTVFGLYQQLSSS-----SSAAVDIKASDL 183
DB 206 SEAILNLIKHPGM--VWVGAIADDDYGVKTKFKKEMESANLVAFSFETIPKVSNEK 263
QY 184 PQSDQVNDKITOK-----YRTILDSTVVASQREYINSYVQKQPI 224
DB 264 MQKAVKAVKSTAVIVLYTSDIDLSPVLEMIHNITDRTWATE-AWITSALIAKP-- 320
QY 225 NYV-----GVYSMCEI---KDIIRDOQ-----YN 247
DB 321 EYFYPGGTIGFAIPRSVITGLKEFLYDVHPNDPNDVLTIEFWQTAFNCTWPNSSVYN 380

QY 248 ----VOLIGTSKPYVYTDVLAALNSLDCDEKQVAVEVIAKULLNTVLDLIGLIT--- 300
Db 361 VDHRRNMGMKEKEDRLYDMSD-----OLCTGEK--LELDKN-----TYLDTSQRLRITKQC 427
QY 301 ---LPANKNGIAHLAK 313
Db 428 KQAVYAIHAGLDHLSR 443

RESULT 11

024399 PRELIMINARY; PRT; 448 AA.
ID 024399
AC 024399
DT 01-JUN-1998 (TREMBlrel. 05, Created)
DT 01-JUN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Fibrin/plasmin-like (Fragment).
OS Triticum aestivum (wheat).
OC Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, VICTORY; TISSUE=ROOT;
RX MEDLINE=97422889; PubMed=9276954;
RA Cruz-Ortega R., Cushman J.C., Ombry J.D.;
RT "cDNA clones encoding 1,3-beta-glucanase and a fibrin-like
RT Plant Physiol. 114:1453-1460(1997)."
DR EMBL; U67717; AAC49613.1; -.
DR HSSP; P13797; IAOA.
DR InterPro; IPR001589; Actbind_actnin.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 4.
DR SMART; SM00033; CH; 3.
DR PROSITE; PS00019; ACTININ_1; UNKNOWN_1.
DR PROSITE; PS50021; CH; 3.
FT NON TER 1
SQ SEQUENCE 448 AA; 50505 MW; 3C0A39B8DA808C7 CRC64;

Query Match 6.0%; Score 109; DB 10; Length 448;
Best Local Similarity 20.7%; Pred. No. 19;
Matches 77; Conservative 72; Mismatches 155; Indels 68; Gaps 17;

QY 16 LPSNNGNGEVYKILNLIKDV-----LPTQVSSVNIETFEPCDYSASIQS 60
Db 5 LNPWRNENHNLCLNSAKAIGCTVNVIGTQFLVEGRPHLVGLISQITIKIQLLADNLKK 64
QY 61 LPDVFS--TDSIFLPYLVSLGVKSLDESLVR-----GVTDLHSPVSSASVNGS 109
Db 65 TPQVELPDDSKDIDEVLSTL-----STERKMLRWNNHLLKKXGKKTANNF--SSDVKGE 118
QY 110 VYGF-----PQYLCNPLSSPNTQOASSLLELAQKVGEQIYVP-DVASSSGFTVFG 162
Db 119 AYAYLLKALAE-TSPETTLERKNPDERAKWLEQAERKIDCRKRYLTPKDITEGSANTLMA 177
QY 163 LYQQLSSSSAAVDIKASDLPQSGDVNKDITOK---YRTILDSTVVASQREYINSVKQ 219
Db 178 FVAQIFQRNGITSDIKQVTTLTQASRPDVLSREERAFRMKNTSLGES--YNNVFE 234
QY 220 GKPSINYYGVSESMCEIKDIIIRDQYVVOVLIGTSDEKPYVYTDVLAALNSLDCDEKQYAV 279
Db 235 --DVANGV-----LLEVLDKVSPSSVWKL---ESKRPILKPFKLEN--CNQVYKIGK 282
QY 280 EV---IKVLLNTVYL--DLGLGLTPANKNGIAHLAKSSNFYQSLSQQDPAKSEVVR 334
Db 283 ELKESLVNLAGNDIVQGNKKLIVALLMQIMRFNIIQLNRLSRSHSGSGQKQITADI-- 340
QY 335 LRCVDPAKEVK 346
Db 341 ---LNMANSKVK 349

RESULT 12

044800 PRELIMINARY; PRT; 998 AA.
ID 044800
AC 044800
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE F14D2.6 protein.
GN F14D2.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copesey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Larrelle P.,
RA Ligniting J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterson R.,
RA Watson A., Weinstock L., Wilkinson-Spratt J., Woldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Du Z., Le T.T.;
RT "The sequence of C. elegans cosmid F14D2.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF040643; AAB94960.1; -.
DR InterPro; IPR000494; EGFR_L_domain.
DR Pfam; PF01030; Recep_L_domain; 3.
SQ SEQUENCE 998 AA; 113094 MW; BA48A4E614F90D1B CRC64;

Query Match 6.0%; Score 108.5; DB 5; Length 998;
Best Local Similarity 22.6%; Pred. No. 64;
Matches 76; Conservative 56; Mismatches 125; Indels 79; Gaps 17;

QY 8 LTVGLFPLPSNNGNGEVKILNLIK-DV-LPTQVSSVNIETFEPCDYSDA-----SLQ 59
Db 137 LRTSYNSIDWWSQETSKWMDINNTKLDVGICVCAARDI-YAFNPNYGNKKVVAADSYK 195
QY 60 SLDPVFETDSIFLPYLVSLGVKSLDESLVRGVG-DLHSPVSSASVNGSVGFPO-YL 117
Db 196 STTQGFPTIQALQYLSLSLTKKLNGLMRYETGLENVFLEGLERHNGNGSLPKEYW 255
QY 118 CSNF--LSSPNTQOASSLLELAQKVGEQIYVPDVASSSGFTV-----FGLYQQL 167
Db 256 SFNFTSIHDNN-----LRRIGLDSL--KQGPAGKFTIIRANNHPDFCLSTSE 302
QY 168 LQSSSSAAVDIKASDLPQSGDVNKDITOK---YRTILDSTVVAS 209
Db 303 LQVAFRNLKIKYGEV-----QICKDLFRDQGTCTCFKLSMLDPKCOHIIQIFINAT 357
QY 210 QREYINSVKGKPSINYYGVSESMCEIKD-----IIRDQ---YNYQLIGTSKPY 258
Db 358 NEEYILNKKNTKYICGFGFGAGFASCYFGEERGVGDILIFSSKLLRNVTLLPQMKPPF 417
QY 259 VYTD--VLAALNSN-----LCDEKQVAVEVIAK 283

Db 418 SPTNPNVIMINNTEQIFQTRACQEFQKFTKSIK 453

RESULT 13

Q20730
ID Q20730 PRELIMINARY; PRT; 528 AA.
AC Q20730;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE F53F4.5 protein.
GN F53F4.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Petioderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RN [2]
RM Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
RX MEDLINE=9069613; PubMed=9851916;
RA none;
RT "genome sequence of the nematode C. elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; 277663; CAB01214.1; -
DR InterPro; IPR000960; Flav_cont_mnoxn.
DR Pfam; PF00743; FMO-1like; 1.
SQ SEQUENCE 528 AA; 60119 MW; C6261F9BFE37CE20 CRC64;

Query Match 6.0%; Score 108; DB 5; Length 528;
Best Local Similarity 21.7%; Pred. No. 28;
Matches 59; Conservative 47; Mismatches 80; Indels 86; Gaps 15;

Qy 43 YNIEYEDCYSDASLQSLPVSFTSIFLPLV-----SLGVK----- 82
Db 238 YDVL--FSRYDYLTKIPIHAVAND--FMERYLQGRMDHYGKRPFRFOQHPTND 293
Qy 83 SLDSLVRG--VTGDLHSFVSSASVNGS-----VYGPQYLCNFISS 125
Db 294 ALANLTCAGYITTEDIDFTENSIVYVKGREPKDIFLTCTGYTFGFP-----FV--- 344
Qy 126 PNGQOASLLELA-QKVGQIVYPDVASSSFTVFLYQOL-----LQSSSAAY 176
Db 345 -----DSDIYEIKNQVPLKYVFP--PNSDVAVIGLIQIPISIAISEIQRMARV 396
Qy 177 DIKASDLPOSGDQVNDITQKVRTLDSTVVASQREYINSVKQGPISNYVGYSESWE 236
Db 397 FAGCGQLPSSGEQID-DIQR-----KAMMKRYRDSIKH--TIQVDYMSYDEIAE 445
Qy 237 IKDIIRDOVN-----VOLIGTSKPYVY 260
Db 446 IIGCLPMKHYLFYPRFMKLFMGANVPYAY 477

RESULT 14

Q9HJ37
ID Q9HJ37 PRELIMINARY; PRT; 2081 AA.
AC Q9HJ37;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE Conserved hypothetical membrane protein.
GN TAI136.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermophilic scavenger Thermoplasma
acidophilum."
RL Nature 407:508-513(2000).
RL EMBL; AL445066; CAC12262.1; -
KM Complete proteome.
SQ SEQUENCE 2081 AA; 227495 MW; 6E02AA6470DB2E8D CRC64;

Query Match 5.9%; Score 107; DB 17; Length 2081;
Best Local Similarity 19.8%; Pred. No. 2,3e+02;
Matches 77; Conservative 59; Mismatches 148; Indels 104; Gaps 15;

Qy 15 YLPSMNENGVKILNLIKDVLPYQVSGNIEYEFPCYSDASLQSLPVSFTSIFLP- 73
Db 1102 YVP-----MNTINLALSLQGVNLGFSI-YVNGTAYSNSTYKN-----GHYLYLPS 1147
Qy 74 --YLVSLGVKSLDESIVRGVGTGLHSFVSSASVNGSVYGFPOYLCSNFLSSPNTQQ 131
Db 1148 GNYTISARSSNATTDSDIYVLP--WNSFVAVSLPYKAV-----RVSGTAS 1192
Qy 132 ASSLELQKVGVEQI-----YYPDVASSSFTVFL--YQQLQSSSAVADIK 179
Db 1193 NISWIKFLSGNNGVAVSVNTTGVPSVIVPAGTVYVYGQGFAPLKTITLSTNDIN 1252
Qy 180 ASDLPQSGDDVNDIT-----YYPDVASSSFTVFL--YQQLQSSSAVADIK 206
Db 1253 ISGVPAATVSLSENITNIVSSGYSIVSSGSPFIYTYSSGSGFSLPSGYTITVAST 1312
Qy 207 VAS-----QREYINSVKQGPISNYVGYG--ESMCEIKD-IIRDOVN 247
Db 1313 IAGSYSSILKLPRTKSVSQMHVNSTMGFVLYNAGISSSVSNVSDGYMLXSYG 1372
Qy 248 VOLIGTSKPYVYTDVIALNSNLCDERQKVAVEYIKNLINTLVLLGLGLTPANKG 307
Db 1373 IPVAVPINSQGYTDIYVAPNIGSPKIEIISPDYNTLTN--ISSAMTIGLT-PMNVPV 1429
Qy 308 IAHAKSSNF-----YVQSLQSPDAKES 330
Db 1430 TITLYNSSRLAVFSGVAVLQGTVDYKLS 1457

RESULT 15

Q9F4J3
ID Q9F4J3 PRELIMINARY; PRT; 1007 AA.
AC Q9F4J3;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PBLA.
GN PBLA.
OS Streptococcus mitis phage SM1.
OC Viruses.
OX NCBI_TaxID=157924;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21116945; PubMed=11179301;
RA Bensing B.A., Rubens C.E., Sullam P.M.;
RT "Genetic loci of Streptococcus mitis that mediate binding to human
platelets."
RL Infect. Immun. 69:1373-1380(2001).
DR EMBL; AY007505; AAC18638.1; -
SQ SEQUENCE 1007 AA; 107445 MW; E568CF7E242A792 CRC64;

Query Match 5.9%; Score 106.5; DB 9; Length 1007;
Best Local Similarity 21.3%; Pred. No. 88;
Matches 78; Conservative 53; Mismatches 114; Indels 121; Gaps 20;

Qy 90 RGVGTGLHSFVSSASVNGSVYGFPOYLCSNFL-----LSSPNTQ 130
Db 17 RGITGKIQSLINPEASAGSAG--QSLGSSLVGVMTKVIAAAGIKAFSAISGALQ 74

```

QY 131 QASSLLEI-----AQV-GYEQIYPPDVASSSSF---TVFGLYQQLIQS---SSSAVADI 178
Db 75 QSLGIEFTLFRGSADKVGANBEAKTGLSANAYMENVTGFSASLLQSLGDDTNKAAET 134
QY 179 KASDLPOSGDQVNDITQKRTILDSTVVASQREYINSVKOG-KPISNYVGYSESMEI 237
Db 135 ANMAMIDMSDNANK-----MGTSMESIOMAYQGFQKQNTYMLDNLKLGYGGTQDEM 185
QY 238 KDIRDQO-----YVQLIGTSDKPYVYTDVLALNSNL-----CDEKQ 275
Db 186 QRLADAEKLTGVKYDIN--NLSD---YSAIHAIQENLDITGTAKERAASTFGSGFESM 240
QY 276 KVAVEVI-----KNLL-----TNTLVLD-----LLGLGLTPANKNGIAH 310
Db 241 KAAQNVVLGKLALGENILPSLHALLKTSTFLFDMFLPMIGNVFSGLGLVL--TEGISQ 297
QY 311 LAK-----SSNRYAQISQ-----QFD-----AKESEVRVLRCDVPFANK--EYKN 347
Db 298 IASQLFGDAFGSAVFDQLSRITGIFETFFDMLFGSLSKQDNIDILNTIGFSEEAATQIVN 357
QY 348 CAGVLR 353
Db 358 IADNIR 363

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Search completed: January 24, 2003, 19:42:43
 Job time : 41 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: January 24, 2003, 19:37:39 ; Search time 14 Seconds
(without alignments)
1054.684 Million cell updates/sec

Title: US-09-675-509-4

Perfect score: 1802
Sequence: 1 MSTOPKTLVGLPEPLPSMN.....CVDPANKEVKNAGVLRPL 356

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	230	12.8	409 1	THI1_PANTH
2	115.5	6.4	886 1	APCE_PORPU
3	111.5	6.2	2670 1	YA05_SCHPO
4	108	6.0	885 1	APCE_AGLNE
5	104.5	5.8	512 1	AMY1_DEBOC
6	104	5.8	689 1	BCSB_PSEPL
7	101	5.6	1042 1	SVI_EORBU
8	99.5	5.5	701 1	VAB5_SCHPO
9	98.5	5.5	1160 1	C8CA_BACTP
10	97.5	5.4	1111 1	KIP1_YEAST
11	97.5	5.4	2701 1	IP3S_HUMAN
12	97	5.4	525 1	DIMH_CABEL
13	96.5	5.4	793 1	YHCD_ECOLI
14	96.5	5.4	889 1	COPP_YEAST
15	96	5.3	485 1	Y045_MYCPN
16	95.5	5.3	809 1	ENPL_HORVU
17	95.5	5.3	1324 1	CUT3_SCHPO
18	95	5.3	1098 1	PROF_MAIZE
19	94.5	5.2	394 1	LIP3_DROME
20	94.5	5.2	466 1	SVN_YERPE
21	94.5	5.2	1125 1	YE62_SCHPO
22	94.5	5.2	1868 1	YHDO_YEAST
23	94	5.2	408 1	AROA_SULTO
24	94	5.2	676 1	IF2M_YEAST
25	94	5.2	776 1	AKH6_HUMAN
26	94	5.2	1285 1	TOXA_PASNU
27	93.5	5.2	346 1	CG2A_DAUCA
28	93	5.2	346 1	P8TS_ECOLI
29	93	5.2	406 1	PKK3_HUMAN
30	93	5.2	626 1	RROC_SYNY3
31	93	5.2	1104 1	STV_YEAST
32	92.5	5.1	279 1	PHEA_LACLA
33	92.5	5.1	429 1	RNE_GUTH

34	92.5	5.1	513 1	XYLG_ECOLI	P37388	escherichia
35	92.5	5.1	662 1	TLPB_BACSU	P39217	bacillus su
36	92.5	5.1	1177 1	Y307_MYCGE	P47549	mycoplasma
37	92.5	5.1	4385 1	YP73_CABEL	009222	caenorhabdi
38	92	5.1	348 1	MO2L_ARATH	092277	arabidopsis
39	92	5.1	551 1	YGIF_YEAST	P53214	saccharomyc
40	92	5.1	3562 1	PGCV_CHICK	090953	gallus gall
41	91.5	5.1	376 1	MID2_YEAST	P36037	saccharomyc
42	91.5	5.1	402 1	METK_PYRAE	082977	pyrobaculum
43	91.5	5.1	529 1	TCPB_CABEL	P47207	caenorhabdi
44	91.5	5.1	531 1	NUSA_MYCGE	P47387	mycoplasma
45	91.5	5.1	896 1	APCE_SYNY4	002907	synecocyst

ALIGNMENTS

```

RESULT 1
THI1_PANTH STANDARD; PRT; 409 AA.
ID      1
AC      P45741;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Thiaminase I precursor (EC 2.5.1.2) (Thiamine pyridinylase).
OS      Paenibacillus thiaminolyticus (Bacillus thiaminolyticus).
OC      Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX      NCBI_TaxID=49283;
RN      [1]
RP      SEQUENCE FROM N.A., AND SEQUENCE OF 31-50.
RX      MEDLINE=96216437; PubMed=8631946;
RA      Costello C.A., Kelleher N.L., Abe M., McLaflerty F.W., Begley T.P.;
RT      "Mechanistic studies on thiaminase I. Overexpression and
RT      identification of the active site nucleophile.";
RL      J. Biol. Chem. 271:3445-3452(1996).
RN      [2]
RP      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX      MEDLINE=99060077; PubMed=9843405;
RA      Campobasso N., Costello C.A., Begley T.P., Ealick S.B.;
RT      "Crystal structure of thiaminase-I from Bacillus thiaminolyticus at
RT      2.0-A resolution.";
RL      Biochemistry 37:15981-15989(1998).
CC      -1- FUNCTION: DEGRADATES THIAMINE BY REPLACING ITS THIAZOLE MOIETY WITH
CC      A WIDE RANGE OF NUCLEOPHILES.
CC      -1- CATALYTIC ACTIVITY: Thiamine + pyridine = heteropyrithiamine + 4-
CC      methyl-5-(2-hydroxyethyl)-thiazole.
CC      -1- SUBUNIT: MONOMER.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- INDUCTION: INHIBITED BY ORGANOMERCURIALS AND IODOACETATE.
CC      -1- MASS SPECTROMETRY: MW=42127; MW_ERR=1; METHOD=Electrospray;
CC      RANGE=31-409.
CC      -1- MASS SPECTROMETRY: MW=42198; MW_ERR=1; METHOD=Electrospray;
CC      RANGE=30-409.
CC      -1- MASS SPECTROMETRY: MW=42255; MW_ERR=1; METHOD=Electrospray;
CC      RANGE=29-409.
CC      -----
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CC      entities requires a license agreement (See http://www.isb.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U17168; AAC44156.1; -.
DR      PDB; 2THI; 07-OCT-98.
DR      PDB; 3THI; 14-OCT-98.
DR      PDB; 4THI; 14-OCT-98.
DR      InterPro: IPR000567; SBP_bac.1.
DR      Pfam: PF01547; SBP_bacterial_1; 1.
KW      Transferrase; Signal; Thiamine catabolism; 3D-structure.
FT      SIGNAL 1 29
FT      CHAIN 30 409 THIAMINASE I.

```

Query Match	12.8%	Score 230;	DB 1;	Length 409;
FT ACT_SITE	143	143	NUCLEOPHILE.	
FT ACT_SITE	271	271	BASE.	
FT VARIANT	30	30	MISSING (IN PART OF THE CHAINS).	
FT VARIANT	31	31	MISSING (IN PART OF THE CHAINS).	
FT MOTAGEN	143	143	C-S. INACTIVATES ENZYME.	
FT MOTAGEN	271	271	E->Q. LOSS OF ACTIVITY.	
SO SEQUENCE	409 AA;	45213 MW;	9A5BD986C5C9182A CR064;	

Query Match	12.8%;	Score 230;	DB 1;	Length 409;
Best Local Similarity	25.2%;	Pred. No. 5.1e-09;		
Matches 90;	Conservative 53;	Mismatches 146;	Indels 68;	Gaps 14;

Qy	7	TLTGLFPEYLSMNGEVEVLINLIKGVLTQVSGNIEKTEEDCQSDASLSGLPVSF	66
Db	40	TLKVAIYYVP-----DPAFQAAVLDQMRQREBPVKYLETDMDSISADPDDL-DVEV	92
Qy	67	TDSIFLPALVSLG-----GVKSLDESILRVGTDLHGFVSSASVNGSVYGFPOYLCSNF	121
Db	93	LDSIFLSHFVDAGYLLPFGSODIDQ-----EVLFPALQAGARNREYVGLPOLICTNL	146
Qy	122	LLSPNGTQ--QASLLELAQVKG---YEQIVYDP-----VASSSPFLVGLYQOLLQSS	171
Db	147	LFYRGGDLKIQGVNDIYYLYKKIGTSHSEQLPFPQNGGLINMAGGTTKASMTLE----	201
Qy	172	SSAAVDIKAS---DLPOSQGVNKDITQKYRTLLDST-----VVASOREYINSVKQG	220
Db	202	--ALDVTGQVTEYDLRPLRLPLNDKVIIRGLRLINMAGEKPSQVYVEDGAVYRASWFA	258
Qy	221	KPISNYVYVYGESMECEIDILRDQVYNOLLGTS---DKPVLVYDIALNLSLDCDEKQV	277
Db	260	QGSGRAPFGYESMNRMDYA--EQVRKRPISSSAGODILFEDVYDVANSKTNHP----	313
Qy	278	AVEYIKNLITNTLVLDLIGLGL-----TLPAKNGCIAMHLAKSNFYAOLSQ	323
Db	314	--ELAKKLIANWASADYEQALRPQADQVQYLLRPHQVYUEALMDYRYSLEAQ	368

RESULT 2	
APCE_PORPU	
ID _APCE_PORPU	STANDARD;
	PRT; 886 AA

DT 01-JAN-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Phycobilisome linker polypeptide (Anchor polypeptide (PBS-anchor protein)).
GN APEC.
GN Porphyra purpurea.
GN Chloroplast.
GN Eukaryote.
GN Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra

RN
 (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Avonport;
 RA Reith M.E., Munnholland J.;
 RT "Complete nucleotide sequence of the *Porphyra purpurea* chloroplast
 RI genome.";
 RL Plant Mol. Biol. Rep. 13:333-335(1995).

CC -1- FUNCTION: THIS PROTEIN IS POSTULATED TO ACT BOTH AS TERMINAL
CC -1- ENERGY ACCEPTOR AND AS A LINKER POLYPEPTIDE THAT STABILIZES
CC THE PHCOBLISOME ARCHITECTURE.
CC -1- SIMILARITY: OF THE REPEATED DOMAINS TO N-TERMINAL REGIONS OF
CC PHYCOCYANIN ROD LINKER POLYPEPTIDES.

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EMBL; U38804; AAC08149.1; -.

DR HSSP; P00315; 1B33.
DR InterPro; IPRO01297; PBS linker poly.
DR InterPro; IPRO01659; Phycobiosome.
DR Pfam; PF00427; PBS linker poly; 3.
DR Pfam; PF00503; Phycobiosome; 1.
DR Pfam; PF00034; Phycobiosome; 2.
DR Phycobiosome; Electron transport; Photosynthesis; Repeat.
KW Chloroplast. 866 AA; 100160 MW; B21074C6D58C6203 CRC64;
SQ SEQUENCE

Q	SEQUENCE	886 AA;	100160 MW;	B21074C6D58C6203 CRC64;
Query Match		6.4%	Score 115.5;	DB 1; Length 886;

Matches	75; Conservative	57; Mismatches	124; Indels	109; Gaps
QY	54	SDASIQSLPDYFSTDSIFLPLVLSLG-GVKSLSDESLVRGVTGDL-----	HSFVS--SS	103
Db	521	SSANFENSVDVIAKVS-----YLRFVGEVNVQEEQLTLPRLESQLODQGISVREFIRQLAK		
QY	104	ASVNGSVYGFQYVICS-----NFLSSPN-GTQOASLSLELAKVGEYQIYVPDVASS		156
Db	577	SIIFSLSIWEPLIYICKALEYIHNRLGRPTYGROEINKYFDIAKESYQVVDAILDSPE		636
QY	157	SETVFG-----LYQQLLOSSSAVADI-KASDLPQSGD		188
Db	637	YIEFTGENVPEERYTTPAGIALRLSPGIIIDQFKKVISSKSRFVELKVKKEIRSSND		696
QY	189	-----QVKNKITOKYRTILDSTVVAQREI-----INSVQGRKISN		225
Db	697	IQRIAQGVLTALRQSVIFDVNONSQE-----VLEQALRAAYRQIFERDILMSFSIGGEFLD		753
QY	226	YVVGSESMCEIKIILRD-----QQY-NVQLIGTSDK-----PYVYTDVLA		266
Db	754	IESSTLNQINQVKEIQLQALSELSELYGKEFQPYRNTKVIIEGTGHLIGRAPRNNOAQEIRFL		813
QY	267	NSNLCDEKQKVAVEIKNLT-----TNFLVLDLGLGLTLTPANKNGIAHLAKSSNFYA		319
Db	814	NQILASKGLSTFVETLVNSSEYDSVYGTNTVPEYRFP-----ANFPTETFLYN		865
QY	320	QLSQQ	324	
Db	866	RLTKQ	870	

RESULT 3	
YAQ5_SCHPO	
ID_YAQ5_SCHPO	STANDARD; PRT; 2670 AA

AC Q10103
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Putative transcriptional activator C18G6.05C (GCN1 homolog)
 GN SPAC18G6.05C
 OS Schizosaccharomyces pombe (Fission Yeast)
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces
 OX NCBI_TaxID=4896;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandrem M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgours J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks, Brown J., Brown S., Chillingworth I., Callicott J. M.,
RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gellies S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Hentley S., Hornsby T., Howarth S., Huckle E. J., Hunt S., Jørgels K.,
RA Jones K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M. A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R. G., Tivey A., Walsh S. V., Warren T., Whitehead S.,
RA Taylor K., Tivey A., Walsh S. V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
 RA Willems I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moesli D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wandt R., Pinnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shipakovski G.V., Usery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of *Schizosaccharomyces pombe*."
 RL Nature 415:871-880(2002).
 CC -1- SIMILARITY: STRONG, TO YEAST GCN1.
 CC -1- SIMILARITY: CONTAINS 19 HEAT REPEATS.
 CC -----
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 CC -----
 DR EMBL; Z68198; CAA92385.1; -
 DR InterPro; IPR000357; HEAT_repeat.
 DR Pfam; PF02985; HEAT_4.
 DR PROSITE; PS50077; HEAT_REPEAT; 4.
 KW Hypothetical protein; Translation regulation; Activator; Repeat.
 FT REPEAT 315 352 HEAT 1.
 FT REPEAT 1062 1099 HEAT 2.
 FT REPEAT 1319 1356 HEAT 3.
 FT REPEAT 1439 1476 HEAT 4.
 FT REPEAT 1478 1514 HEAT 5.
 FT REPEAT 1518 1555 HEAT 6.
 FT REPEAT 1557 1593 HEAT 7.
 FT REPEAT 1637 1674 HEAT 8.
 FT REPEAT 1676 1713 HEAT 9.
 FT REPEAT 1714 1751 HEAT 10.
 FT REPEAT 1753 1792 HEAT 11.
 FT REPEAT 1793 1830 HEAT 12.
 FT REPEAT 1898 1939 HEAT 13.
 FT REPEAT 1941 1977 HEAT 14.
 FT REPEAT 1982 2019 HEAT 15.
 FT REPEAT 2020 2055 HEAT 16.
 FT REPEAT 2057 2090 HEAT 17.
 FT REPEAT 2319 2361 HEAT 18.
 FT REPEAT 2379 2416 HEAT 19.
 S1 SEQUENCE 2670 AA; 297333 MW; 948E9316D56D74C3 CRC64;
 Query Match 6.2%; Score 111.5; DB 1; Length 2670;
 Best Local Similarity 19.7%; Pred. No. 15;
 Matches 77; Conservative 60; Mismatches 146; Indels 107; Gaps 17;
 QY 10 VGLF-----PILP-----SNENGENEVLINL-----IDVLPVTOGSGNI 45
 Db 1433 LGIFFEPLPLPLTLTSFGDNANEVREATMDAVKQIMSQLSAFGVLLPLTLIDGLN- 1491
 QY 46 EYTFEDCVSDASLQSLPDVFTD--SIFLPYLVISGVKSLDESIVRGVTDLSHFVSS 103
 Db 1492 EYNNRSKASVEILGLMSYMAPKQLSVFLPTI-----IPKLSVLT-----DSMSQVANT 1541
 QY 104 ASVN---GSYGRP--OYLCSNPLSSPNGTQOASLLELAQKVGEOIVYPDV---- 152
 Db 1542 ANKSLRFRGDVINSPEIQTLPTLLKALSDCTRYTDALFALLKTSFVHYLDPSLALVI 1601
 QY 153 -----ASSSFTVFGLYQQLQSSSSAAV-----DIRASD 182
 Db 1602 PILKYGLERNAGTRQQAQKIFGLMASTREPENLAVYESLMPRLREVLDPVDPTRATA 1661
 QY 183 LPSGDQVNDKITQKRYTILDS--TVVASQREYINSVKGQRISSVYVYGSESMCE--IK 238

Db 1662 AKALGSIEIKGEKKEPTLIPELFNVRISCESEVDROGAAGSEIIAGLARLEDPVP 1721
 QY 239 DIIRDOQ-----YVQIGTSDPKPYVTDVIALNSLDCDEK---QKVAVE 280
 Db 1722 EILKNTSSPPPHIRESTISLILYLPATFGSRFPQYLARALPILSLGLADSELVQTASLR 1781
 QY 281 VIKNLTN--TLVLDLIGLGLTTPANKGT 308
 Db 1782 AAKMIVNVATKSYVDLL-----LPELEKGL 1806
 RESULT 4
 APCE_AGLINE STANDARD; PRT; 885 AA.
 ID APCE_AGLINE
 AC P2856;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Phycobillosome linker polypeptide (Anchor polypeptide) (PBS-anchor
 DE protein).
 GN APCE.
 OS Aglaetochamion neglectum.
 OG Chloroplast.
 OC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Ceramiales;
 OC Aglaetochamion.
 OX NCBI_Taxid=2765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93144689; PubMed=7678762;
 RA Apt K.E., Grosman A.R.;
 RT "Characterization and transcript analysis of the major
 RT phycobilliprotein subunit genes from *Aglaetochamion neglectum*
 RT (Rhodophyta)."
 RL Plant Mol. Biol. 21:27-38(1993).
 CC -1- FUNCTION: THIS PROTEIN IS POSTULATED TO ACT BOTH AS TERMINAL
 CC ENERGY ACCEPTOR AND AS A LINKER POLYPEPTIDE THAT STABILIZES
 CC THE PHYCOBILISOME ARCHITECTURE.
 CC -1- SIMILARITY: OF THE REPEATED DOMAINS TO N-TERMINAL REGIONS OF
 CC PHYCOCYANIN ROD LINKER POLYPEPTIDES.
 CC -----
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 CC -----
 DR EMBL; Z11905; CAA77957.1; -
 DR PIR; S20621; S20621.
 DR HSSP; P00315; 1B33.
 DR InterPro; IPR001297; PBS_linker_poly.
 DR InterPro; IPR001659; Phycobillosome.
 DR Pfam; PF00427; PBS_linker_poly; 3.
 DR Pfam; PF00502; Phycobillosome; 1.
 DR Pfam; PD000340; Phycobillosome; 2.
 KW Phycobillosome; Electron transport; Photosynthesis; Repeat;
 KW Chloroplast.
 S1 SEQUENCE 885 AA; 101153 MW; C91D75CD6307B4B9 CRC64;
 Query Match 6.0%; Score 108; DB 1; Length 885;
 Best Local Similarity 21.2%; Pred. No. 5.5; 119; Indels 104; Gaps 21;
 Matches 79; Conservative 70; Mismatches 119;
 QY 53 YSDASLQSLPDVPS--TDSIFLP-----YLVSLGVKSLDESIVRGVTDLSHFVSS--S 103
 Db 518 FSDEWMLPDIIEGIIKATILRVFGRTIYELSSVAKF--ESLFRSSEKISVDPRIARLVK 576
 QY 104 ASVNGSYVGPYQYCSNF-----LSSPN--GTQOASLLELAQKVGEOIVYPDVAVSS 156
 Db 577 SSVFRSLYWEPLIYCAIKAEIYHYVLLGRPSYGRQEIINQYDIIVREGYIMIDYLLNSSE 636
 QY 157 SFTVFG-----LYQQLQSSSSAAVDIRASDL--PQSGDQV 190

Db 637 YIRSGDNTPVERKITSANMILSNYSNPLSTLTKTNSKSKFTELSTLEKSLMSI 696
Qy 191 NKDITOKRYTILDS-----TVVASQ---REYINSVKO---GKPSINYVGSSESMCB-- 236
Db 697 QARISQSGVSTYRDQYKVPQLTQSSQVVKQVAKIYQIREFRLNSALIGDEFINLEKA 756
Qy 237 -IKUIIRDQYNVOLIGTSD-----KPYVYTDVLALN-----SNLCEK--OK 276
Db 757 LVNNNITVQOF-IEQIGSSSYGRFPYPPNTKVIELGTGKFLGRAPNNOAIEIRYNOI 815
Qy 277 VAVETIKKLNTLTVL-----DLGGL-----TLPAKNCIAHLASSNRYAQLS 322
Db 816 LASQGLSSFFIT--VLVNSNEYNOVGVNIIVYRRFTLLPA-----ANPMTKLYNTLT 867
Qy 323 QOFDAKESSEVRV 334
Db 868 KQ---SSEITV 875
AC P19263; STANDARD; PRT: 512 AA.
ID AMYL DEBOC
AC 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AMYL.
OS Deacryomyces occidentalis (Yeast) (Schwanniomyces occidentalis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=27300;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 26076;
RX MEDLINE=90032659; PubMed=2806251;
RA Strasser A.W.M., Selk R., Dohmen R.D., Niermann T., Bielefeld M.,
RA Seebach P., Tu G., Hollenberg C.P.;
RT "Analysis of the alpha-amylase gene of Schwanniomyces occidentalis
and the secretion of its gene product in transformants of different
yeast genera.";
RT Eur. J. Biochem. 184:699-706 (1989).
RL [2]
RN SEQUENCE FROM N.A.
RC STRAIN=CCRC 21164;
RX MEDLINE=92120467; PubMed=1769525;
F Mu F.M., Wang T.T., Hsu W.H.;
R "The nucleotide sequence of Schwanniomyces occidentalis alpha-amylase
gene.";
RT FEBS Microbiol. Lett. 66:313-318 (1991).
RL [3]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 26077 / CBS 2863;
RX MEDLINE=92307400; PubMed=1612414;
RA Park J.C., Bai S., Tai C.Y., Chun S.B.;
RT "Nucleotide sequence of the extracellular alpha-amylase gene in the
yeast Schwanniomyces occidentalis ATCC 26077.";
RL FEBS Microbiol. Lett. 72:17-23 (1992).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- ENZYME REGULATION: ALPHA-AMYLASE EXPRESSION UNDERLIES CATABOLITE
CC REPRESSION BY GLUCOSE.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
DR EMBL; S77586; AAB21151.2; -
DR EMBL; X16040; CAA34162.1; -
DR EMBL; X62079; CAA43995.1; -
DR EMBL; S38381; AAB22383.2; -
DR PIR; S06115; S06115.
DR PIR; S23355; S23355.
DR HSSP; P10529; 7TAA.
DR InterPro: IPR000461; Alpha amylase.
KW Hydroxylase; Glycosidase; Carbohydrate metabolism; Calcium;
KW Glycoprotein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 512
FT ACT_SITE 242 242
FT ACT_SITE 246 246
FT ACT_SITE 333 333
FT CARBOHYD 233 233
FT DISULFID 66 74
FT DISULFID 186 200
FT DISULFID 276 319
FT DISULFID 475 510
FT VARIANT 32 32
FT VARIANT 36 36
FT VARIANT 73 73
FT VARIANT 280 280
FT VARIANT 350 350
FT VARIANT 479 479
FT VARIANT 483 483
FT VARIANT 56527 MM; 857552BCF60965 CRC64;
SQ SEQUENCE 512 AA; 56527 MM; 857552BCF60965 CRC64;
Query Match 5.8%; Score 104.5; DB 1; Length 512;
Best Local Similarity 22.0%; Pred. No. 4.5;
Matches 80; Conservative 48; Mismatches 117; Indels 119; Gaps 21;
Qy 18 SMWNGNEVKLINIKOVLPDQ-----VSGVNIETEPDCYSDASLQSPDVFST 67
Db 160 AMWGDSSVD---YSSFTPEPNOQSYFHDYCLTNNVDQNVEDCMGDTREVSLPDLSTE 215
Qy 68 DS-----IFLPYVSLGCVKSLD---ESLVRGVGTDLHSFVSSASVYV-GSPQYL 117
Db 216 DNEVIGVFQMTWSDPFGVNYGIDGLRISAKHVDPAISLTKFEDASGVYVNGDPTYT 275
Qy 118 C-----SNFLSSP---NGTQOASSLLEAKV-----GYE 145
Db 276 CPYQNYMKGVNTNPLYPVYVRFPSDTSATSS--ELTSMISTLQSSCSGDSVSLGNFIENHD 333
Qy 146 QIVPVDVASSSS-----FTVFG-----LY---QQLLOSSSSAA-----VDIK 179
Db 334 QVRFPSVTSDSLKNDMAFLILGDGIPITYYGQEGQINGSDPANBALWLSGYNTDSE 393
Qy 180 ASDPQSGDQVKNIDITOK---YRTILDSTVVASOREYINSVK----- 218
Db 394 YIELISKNDIQRNARKDKDAYST-YKSSVYSSSDHIATRRKSGDANQLISFNNLSNG 452
Qy 219 -QKPSINYYVGSSEMCERKDIIR-----DOQYNVOLIGTSRKYVYTDVLALNSN 269
Db 453 SQDITVEN--TGVS-SQDKVIDIISCVSLAGDSLSVSISSGMPQVYAFSSVLS-GSG 508
Qy 270 LCDE 273
Db 509 ICNQ 512
RESULT 6
BCSB_PSEFL STANDARD; PRT: 689 AA.
ID BCSB_PSEFL
AC P58934;

DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cyclic di-GMP binding protein (cellulose synthase regulatory subunit).
 OS BCSB OR WSSC.
 OC Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 NC NCB1_TaxID=294;
 RP SEQUENCE FROM N.A.
 RC STRAIN=SBW25;
 RX MEDLINE=22013850; PubMed=12019221;
 RA Spiers A.J., Kahn S.G., Bohannon J., Traviano M., Rainey P.B.;
 RT "adaptive divergence in experimental populations of Pseudomonas
 fluorescens. I. Genetic and phenotypic bases of wrinkly spreader
 RT fitness."; 161:33-46(2002).
 RL Genes 161:33-46(2002).
 CC -1- FUNCTION: Binds the cellulose synthase activator, bis-(3'-5')
 CC cyclic diguanylic acid (c-di-GMP) (By similarity).
 CC -1- SUBUNIT: Tightly associated with the cellulose synthase catalytic
 CC subunit (By similarity).
 CC -1- PATHWAY: Bacterial cellulose biosynthesis.
 CC -1- SIMILARITY: BELONGS TO THE ACSB/BCSB FAMILY.
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 DR EMBL: AY074776; AAJ71843.1; -.
 KW Cellulose biosynthesis.
 SQ SEQUENCE 689 AA; 75272 MW; FBE0B8CE76EF3D8 CRC64;
 Query Match 5.8%; Score 104; DB 1; Length 689;
 Best Local Similarity 21.4%; Pred. No. 7.4;
 Matches 60; Conservative 44; Mismatches 95; Indels 84; Gaps 12;
 QY 14 PY-LPSNNGENVEKILNLIKDVLPYOVSGYN-----I 45
 DB 267 PYDAPNMLPSNRPRVRLGILBIQ-QKLSVSGYNPGAISVDMLPDPDLFWNREGEVPLKLY 325
 QY 46 EYTFDCYSDASLQ-SLPDVSTDSIFLPYIVSLGVKSL-----DSLVKGYTGDLHS 98
 DB 326 RYTPQOVSTVNSSLIGLNDQF-MKSVALLPSVSNLGGGOTLIDOLKDESLPREVT-TLLP 383
 QY 99 FVSSASVNGSVYGFPOYL-----CSNFLSSPNGTQOASSLLEAKVGYEQ----- 146
 DB 384 ISSASPSKQVRFMYDIKCEGCRDIIIVDMKSSVDPDSITLVY---TGQHYIAMPRLG 440
 QY 147 -----IYPPVASSSS-----FTVFGYLQQLQSSSSAAVDIKASDL 183
 DB 441 VFNDGPFPTRLADSSSAVMPDNYGTDELTAIVLTILGARGEANTGATVAKVYQAKDV 500
 QY 184 PQSGDQ-----VNKDITOKYRTILDSTVVASQREYINS 216
 DB 501 QSVADKDLVLATLANOPLRLKMOQOYLPATSDGEHQPLLS 541
 RESULT 7
 SY1 BORBU
 ID SY1 BORBU STANDARD; PRT; 1042 AA.
 AC OS1773;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Isolecyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA ligase)
 DE (1leuS).
 DE ILES OR BB0833.
 OS Borrelia burgdorferi (Lyme disease spirochete).

OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCB1_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
 RA Peterson J., Karpavicz A.R., Quackenbush J., Salzberg S., Hanson M.,
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
 RA Uterback T., Wetchey L., McDonald L., Attiach P., Bowman C.,
 RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 RA Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochete, Borrelia
 RT burgdorferi."; 390:580-586(1997).
 RL Nature 390:580-586(1997).
 CC -1- CATALYTIC ACTIVITY: ATP + L-isoleucine + tRNA(1le) = AMP +
 CC diphosphate + L-isolecyl-tRNA(1le).
 CC -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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 DR EMBL: AE001181; AAC67179.1; -.
 DR HSBP; PE6690; 11LE.
 DR TIGR; BB0833; -.
 DR InterPro: IPR002300; tRNA-synt_1a.
 DR InterPro: IPR001412; tRNA-synt_1.
 DR InterPro: IPR002301; tRNA-synt_1le.
 DR Pfam: PF00133; tRNA-synt_1; 1.
 DR PRINTS; PRO0984; TRNASYNTHILE.
 DR TIGRFAMs; TIGR00392; 1leS; 1.
 DR POSITIVE; PS00178; AA tRNA_LIGASE_I; FALSE_NEG.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Metal-binding; zinc; Complete proteome.
 FT SITE 48 58 "HIGH" REGION.
 FT SITE 594 598 "KMSKS" REGION.
 FT BINDING 597 597 ATP (BY SIMILARITY).
 SQ SEQUENCE 1042 AA; 122331 MW; 6C0P7D820CA32F75 CRC64;
 Query Match 5.6%; Score 101; DB 1; Length 1042;
 Best Local Similarity 18.8%; Pred. No. 22;
 Matches 74; Conservative 59; Mismatches 120; Indels 140; Gaps 16;
 QY 19 WNEGNEVEKILNLIKDVLPYOVSGYNIETPCYSDASLQSLPVDVSTDSIFLPYVSL 78
 DB 634 YSDNG-----VRDLK-----NIIPINWASFTYVAILDKRP-----PKNLST 674
 QY 79 GGVKSLDESIVRGVTDGLHSFVSSASVNGSVYGFPOYLCNFLSSPNGTQOASSLLEL 138
 DB 675 AKNNMLDKWII-----SELSELKK-----ILNTEIDKYNLTKSIESLLEF 714
 QY 139 AKQV-----GYEQIYVPD-----VASSSSFTVFGLYOOLQ 169
 DB 715 IDKLNMYIYRRRRRPFKSNDDKNDAYETLLVYATLMLLAPPIPTTEIYQNLKT 774
 QY 170 SSSSAVDIKASDLPOSQDQ-VNKDITOKYRTILDSTVVASQREYINSVKGQPISNYV 228
 DB 775 DEDQSGIHL--NDYPRKANENFINKITEKINLARKITSMAKSLRLNIRNPISITVI 832
 QY 229 -----GVSESMCEIKDITRDQ-----QYNVOLIGT--SDKRYVY 260
 DB 833 VTKQNQNNMLMEMQETIILDEINAKEMKIKANEELITYAKKANFELGKKLQDKMAVS 892

OY 261 TDV-----LATNSLCEKQKAVVEYK-----N 284
 DB 893 TEISLKNEDIIKIINGSYEIKANAHRYLSLNDIILERREKENLKVINEESTITIGID 952
 OY 285 LITNTVLDTGLGLTPANKNGIAHLAKSNF 317
 DB 953 LITKELIYE-----GLTREFVRO-IONLAKENKF 980

RESULT 8

YABS_SCHPO STANDARD; PRT; 701 AA.
 AC Q09807;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein C2G11.05c in chromosome 1.
 GN SPAC2G11.05c.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_Taxid=4896;
 RN [1]

SEQUENCE FROM N.A.

RA STRAIN=972;
 RA MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA Jones K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skellern J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voiclaert G., Aert R., Robben J., Grymoultier B.,
 RA Wellens J., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Welfens J., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer T., Beck A., Leirich H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Huret S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Snapakovski G.V., Ussery D., Bartell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).

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CC -----
 CC EMBL; Z54354; CA91170.1; -

DR InterPro; IPR004328; BRO1.

DR Pfam; PF03097; BRO1; 1.

KM Hypothetical protein.

SO SEQUENCE 701 AA; 81769 MW; E13E84C4AE085671 CRC64;

Query Match 5.5%; Score 99.5; DB 1; Length 701;
 Best Local Similarity 19.0%; Pred. No. 16;
 Matches 60; Conservative 68; Mismatches 133; Indels 55; Gaps 13;

OY 4 OPKITLVGLFPYLPSEWNGEVEKLIINIKOVLPQVSGNIEYTEPDCYSASLQSLPD 63

DB 309 QPR-IPVGSFPLDT-----VTMVOSTPVDVLDTKTAAPYSTCLDEFFMDLE 357
 OY 64 VFTSDSIFLPYLVISGVKSLDESLVGVGTDLHSFVSSASVNGSVY--GFPQYLCSNF 121
 DB 358 EHEKN-----LIDAAVKSID-CLTKEGTBKLPALMEIKSVNDNNYIETSKWMENF 409
 OY 122 L-ISSPNGTQ---QASLLLEAKV-----GYEQIVPDPVASSSFTYFGLYQOL 167
 DB 410 TEIKNLGLGLEFLRSEASSLCLIDKNGVTRHCCQALDEII-NSVKSQNMKEKGFYSDV 468
 OY 168 LQSSSSAA-VDIKASDLPQSGDQVNVKIDTQKRYTLSTVVASQREYINSVKQKPISNY 226
 DB 469 IKLHEEVSLEKVENENQNAKDITIQKDISAGKQIFELS-AQSERILSNLAEKQNPVTDQ 527
 OY 227 YGVSSEMCETKIDIRDOQVNVQITGTSDDPYV-----YTDTVAL-----NSN 269
 DB 528 LILQANSVLQWDLKDKERNNKTKLGSNDYFNISMYSNHTDHSLLKCFREAVDAKKNFR 587
 OY 270 LCEKQKQKAVVEIKNL 285
 DB 588 RQREORIEIIQWKEKL 603

RESULT 9

C8CA_BACTP STANDARD; PRT; 1160 AA.
 AC Q45706;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pesticidal crystal protein cry8Ca (Insecticidal delta-endotoxin
 DE CryVIIIcA) (Crystalline entomocidal protoxin) (130 kDa crystal
 DE protein).
 GN CRY8CA OR CRYVIII(CA) OR CRYVIII.
 OS Bacillus thuringiensis (subsp. japonensis).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_Taxid=128936;
 RN [1]

SEQUENCE FROM N.A.

RA STRAIN=Butbul;
 RA MEDLINE=94100766; PubMed=7764305;
 RA Sato R., Takeuchi K., Ogiwara K., Minami M., Kaji Y., Suzuki N.,
 RA Hori H., Suzuki N., Ogiwara K., Himejima M., Indrasith L.S.,
 RA Hori H., Asano S., Sato R., Ohba M., Iwahana H.;
 RT "Cloning, heterologous expression, and localization of a novel crystal
 RT protein gene from Bacillus thuringiensis serovar japonensis strain
 RT Butbul toxic to scarabaeid insects.";
 RL Curr. Microbiol. 28:15-19(1994).

SEQUENCE OF 1-14 AND 56-64, AND CHARACTERIZATION.

RA MEDLINE=94259659; PubMed=8200856;
 RA Hori H., Suzuki N., Ogiwara K., Himejima M., Indrasith L.S.,
 RA Hori H., Asano S., Sato R., Ohba M., Iwahana H.;
 RT "Characterization of larvicidal toxin protein from Bacillus
 RT thuringiensis serovar japonensis strain Butbul specific for
 RT scarabaeid beetles.";
 RL J. Appl. Bacteriol. 76:307-313(1994).
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF INSECTS. ACTIVE ON VARIOUS SCARABAEID BEETLES
 CC SUCH AS ANOMALA CUPREA, A. RUFOCUPREA AND POPILLIA JAPONICA.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
 CC THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
 CC TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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 CC -----
 DR EMBL: U04366; AAA21119.1; -
 DR HSSP: P07130; IDLC.
 DR InterPro: IPR001178; Endocoxin.
 DR Pfam: PF00555; endotoxin; 1.
 KM TrkM; Sporulation.
 SQ SEQUENCE 1160 AA; 130425 MW; C16C3D912EB8751 CRC64;
 Query Match 5.4%; Score 98.5; DB 1; Length 1160;
 Best Local Similarity 22.6%; Pred. No. 38;
 Matches 91; Conservative 58; Mismatches 126; Indels 127; Gaps 25;
 QY 26 VKLNLKDVLPVSGVN-----IEYTFD-CYSDASIQSPDVSTSIPLP-YLV 76
 DB VQANLLQDTGFNRINGENGTGTEVEGVDVLFKRSIR-LTSAEIDETETPTL- 785
 QY 77 SLGKSLDESLVRCVGTG-DLHSPVSSASV-----NGSYVGF- 114
 DB 786 ---YQIDESLKPRTYKLGFGSSQDLEIKLIRHRAQIVGVNDLLPVRPVNS 841
 QY 115 -----QYLCNFFLL--SSPNGTQASS-----LLELAQKVGVEQIVVYPDV 152
 DB 842 CGGVDRSGEQYVDANLALENNGENKNSSDSHAFPHITGEIDLENTGI-MIVFKIP 900
 QY 153 ASSSFTVFGLYQQLLOSSSAVADIKASDLPQSGQVN-KDITQKRYTILDSTVASQ 210
 DB 901 TTNGNATLGNL-EFVEEG-----PLSGETLEMAQQEQEQQDMARKRAASE 946
 QY 211 REYINSVKQKGPISNYVYGE---SKCEIKDIIHQVNVOLIGSDKPYVTVDV- 264
 DB 947 KTVY-AAKQA--IDRLFADYQDKLNSGVEMSDLLAQNLT-VQSI-----PYVNDALPE 997
 QY 265 --AANSNLCEKQKVAEVIKNLLTNLT--VLDLGLGLTIPAN--KNGIHLAKSS--- 315
 DB 998 IPGKNVYSFTE-----LTNRLQQAAMLYDLQNALPNDGFRGLSNMNAATSDVN 1045
 QY 316 -----NRYAQLSQQFDKSESEVRLRCVDFPANK 344
 DB 1046 VQQLSDTSVLVTPMNSGVSGQFTVQPRYRVLVLT--ARKK 1085
 RESULT 10
 KIP1_YEAST STANDARD; PRT; 1111 AA.
 ID KIP1_YEAST
 AC P28742;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 D "Kinesin-like protein KIP1."
 GN KIP1 OR CIN9 OR YBL063W OR YBL0504 OR YBL0521.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE=92317166; PubMed=1618910;
 RA Root D.M., Meluh P.B., Rose M.D.;
 RT "Kinesin-related proteins required for assembly of the mitotic
 RT spindle."
 RL J. Cell Biol. 118:95-108(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE=94205266; PubMed=8154187;
 RA Scherens B., el Bakoury M., Vierendeels F., Dubois E., Messenguy F.;
 RT "Sequencing and functional analysis of a 32,560 bp segment on the
 RT left arm of yeast chromosome II. Identification of 26 open reading
 RT frames, including the KIP1 and SECI7 genes."
 RL Yeast 9:1355-1371(1993).
 RN [3]

RP CHARACTERIZATION.
 RC STRAIN=S288C;
 RX MEDLINE=923154062; PubMed=1643659;
 RA Saunders W.S., Hoyt M.A.;
 RT "Kinesin-related proteins required for structural integrity of the
 RT mitotic spindle."
 RL Cell 70:451-458(1992).
 CC -1- FUNCTION: REQUIRED FOR ASSEMBLY OF THE MITOTIC SPINDLE. INTERACT
 CC WITH SPINDLE MICROTUBULES TO PRODUCE AN OUTWARDLY DIRECTED
 CC FORCE ACTING UPON THE POLES. FOLLOWING SPINDLE ASSEMBLY, CIN8 AND
 CC KIP1 APPARENTLY ACT TO OPPOSE A FORCE THAT DRAWS SEPARATED POLES
 CC BACK TOGETHER. THIS FORCE SEEMS TO BE MEDIATED BY KAR3.
 CC -1- SUBUNIT: MIGHT BE DIMERIC.
 CC -1- SUBCELLULAR LOCATION: SPINDLE MICROTUBULES THAT LIE BETWEEN THE
 CC POLES.
 CC -1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BMC
 CC SUBFAMILY.
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 CC -----
 DR EMBL: Z11962; CAA78019.1; -
 DR EMBL: Z23261; CAA80785.1; -
 DR EMBL: Z23824; CAA84883.1; -
 DR PIR: A42640; A42640.
 DR HSSP: P17119; 3KAR.
 DR SGD: S0000159; KIP1.
 DR InterPro: IPR002570; Hpt.
 DR InterPro: IPR001752; kinesin_motor.
 DR Pfam: PF00225; kinesin_1.
 DR PRINTS: PR00380; KINESINHEAVY.
 DR SMART: SM00073; HPT; 1.
 DR SMART: SM00129; KISC; 1.
 DR PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE: PS50657; KINESIN MOTOR DOMAIN2; 1.
 KM Motor protein; Cell division; Microtubules; ATP-binding; Coiled coil;
 KW Mitosis; Cell cycle.
 FT DOMAIN 50 423 KINESIN-MOTOR (BY SIMILARITY).
 FT DOMAIN 424 510 COILED COIL (POTENTIAL).
 FT DOMAIN 648 670 COILED COIL (POTENTIAL).
 FT DOMAIN 710 780 COILED COIL (POTENTIAL).
 FT DOMAIN 808 828 COILED COIL (POTENTIAL).
 FT NP_BIND 141 148 ATP (BY SIMILARITY).
 SQ SEQUENCE 1111 AA; 125794 MW; 212F8279766137FC CRC64;
 Query Match 5.4%; Score 97.5; DB 1; Length 1111;
 Best Local Similarity 21.8%; Pred. No. 42;
 Matches 71; Conservative 50; Mismatches 112; Indels 93; Gaps 15;
 QY 24 NEVKLNLKDVLPVSGVNIETFEPCYSD-----ASIQSPDV-----FSTDS 69
 DB 489 NQDINNLLQSEKELAIQINPNVDFSNF--YSEIQKHHTLLELMEVETIQORDSLEN 546
 QY 70 IFPLVYV-----SLGVKSLDESLVRCVGTGDLHSPVSSASVNG 108
 DB 547 SQKQYNTNQMWQKISQVQLTNTLQGSLLMNYNSKSEYIKGVTELTNNVTHKAKHD 606
 QY 109 SVYGFQYLCNFFLLSPNGTQOASSLLELAQKVGVEQIVVYPDVASSSTVVGCLVQQL 168
 DB 607 STLSKLNITTNLLMNQMN-----ELVRSI-----STSLEIF----- 638
 QY 169 QSSSSAVVDIKASDLPQSGQVKNKITQKRYTILDSTVASQREYINSVYQKRP----- 222
 DB 639 QQSSTSHRYKDLNLEIQSHQFLKLNQNDKSLDLS--IGSILTSINEISQNCCTNLNSM 697
 QY 223 ---ISNYVYGS---ESMCEIK---DIIRDQ---QYVNLIGTSDKPYVTVDLALN 267
 DB 698 NVLIENQSGSSKLKEQDLEIKKLNKDLINERRISGNFQQL--AMKRYFPDHSRTR 755

QY 268 SNLCDEKOKVAEVIKNLINTVLVD 293
DB 756 SEFHDELNK-----CIDNLKDKQSKLD 777

RESULT 11
IP3S_HUMAN STANDARD; PRT; 2701 AA.

AC Q14571; O94773;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Inositol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol 1,4,5-trisphosphate receptor) (Type 2 Insp3 receptor) (IP3 receptor isoform 2) (Insp3R2).
GN ITPR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RA [1]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RX MEDLINE=94363219; PubMed=8081734.
RA Yamamoto-Hino M., Sugiyama T., Hikici K., Mattei M.-G., Hasegawa K., Sekine S., Sakurada K., Miyawaki A., Furuchi T., Hasegawa M., Mikoshiba K.;
RT "Cloning and characterization of human type 2 and type 3 inositol 1,4,5-trisphosphate receptors."
RT Recept. Channels 2:9-22(1994).
RL [2]
RN SEQUENCE FROM N.A. (SHORT ISOFORM).
RC TISSUE=Heart;
RX MEDLINE=98399819; PubMed=9729462;
RA Futatsugi A., Kuwajima G., Mikoshiba K.;
RT N-terminal 175 residues of type 2 Ins(1,4,5)P3 receptor."
RL Biochem. J. 334:559-563(1998).
CC -1- FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, A SECOND MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM/ITPR; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: THE SHORT ISOFORM IS FOUND IN SKELETAL MUSCLE AND HEART.
CC -1- DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.
CC -1- PM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).
CC -1- MISCELLANEOUS: CALCIUM APPEARS TO INHIBIT LIGAND BINDING TO THE RECEPTOR. MOST PROBABLY BY INTERACTING WITH A DISTINCT CALCIUM-BINDING PROTEIN WHICH THEN INHIBITS THE RECEPTOR.
CC -1- SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
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CC
DR EMBL; D26350; BAA05384.1; -
DR EMBL; AB012610; BAA33961.1; -
DR GenBank; HGNC:6181; ITPR2.
DR MIM; 600144; -
DR InterPro; IPR000699; Ca-rel channel.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR000493; Insp3_receptor.
DR InterPro; IPR000636; M-channel_nlg.

DR InterPro; IPR003608; MIR.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF01365; RyR_ITPR; 2.
DR Pfam; PF02815; MIR; 4.
DR PRINTS; PR00779; INSP3RECEPTR.
DR SMART; SM00472; MIR; 4.
KW Receptor; Transmembrane; Glycoprotein; Phosphorylation; Endoplasmic reticulum; Ionic channel; Ion transport; Calcium channel;
KW Alternative splicing.
FT DOMAIN 1 2227 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2228 2248 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 2249 2260 POTENTIAL.
FT TRANSMEM 2261 2281 POTENTIAL.
FT DOMAIN 2282 2307 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2308 2328 POTENTIAL.
FT DOMAIN 2329 2351 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 2352 2372 POTENTIAL.
FT DOMAIN 2373 2394 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2395 2415 POTENTIAL.
FT DOMAIN 2416 2521 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 2522 2542 POTENTIAL.
FT DOMAIN 2543 2701 CYTOPLASMIC (POTENTIAL).
FT MOD RES 2607 2607 PHOSPHORYLATION (POTENTIAL).
FT VARSPIC 176 181 IYVGDK -> DASFWI (IN SHORT ISOFORM).
FT VARSPIC 182 2701 MISSING (IN SHORT ISOFORM).
SQ SEQUENCE 2701 AA; 308074 MW; EB5C7DDCD1F74A CRC64;

Query Match 5.4%; Score 97.5; DB 1; Length 2701;
Best local Similarity 22.6%; Pred. No. 1.5e+02;
Matches 91; Conservative 68; Mismatches 131; Indels 113; Gaps 23;

QY 5 PKLTVLGLFPLPSMNGN---EVKLINLI-----KDLPTQVSGVNIETEF 50
DB 1371 PLAVHITLVELLAACGKGVYTEIKNSLPLDLDIRVAVTHDDCIPE---VKIAVNF 1426
QY 51 --DYSASASQSLPDIYSTDSI---FLPYVSLGV-----KSLDESLVR 90
DB 1427 VNHCVYVTEVE-MEITYTSHIMWLFENFLVDMAVGVNTTDRKHADI FLEKVTESIMN 1485
QY 91 GVTGDLDS-FVSSASVNGSVGFPQYLCSNFLSS---FNGTQOAS-----SLBLAQ 140
DB 1486 IVSFFSPSPSDNSTSQTHQPVFIQLQSAFRVYNTCTWNPQAKAVESCIRTLAEVAK 1545
QY 141 KVGEGQIVPDPVAVSSSFYVGLYQQLQSSSS---AAVDIKASDLPQSGDQVKNDI-- 194
DB 1546 NRG---IAIPVDLDSQVNTLF-----MKSHSNMVQAAAGWRLS--ARSGPRFEKALGG 1594
QY 195 -TQKRYTILD--STVVASQREYINSVQCKRPISVYVYGESEMC--RIKI-IRDOQYV 248
DB 1595 PAMDYRNIEKLDQDVASLHQFSPMMQAEFSLVDVLSPELLPFGSDARIRCGAFWS 1654
QY 249 QLTGTSKPPYVTVLALNSNLCDKOKVAEVIKNLIT-----NTLVLDL- 295
DB 1655 KLINHTKK-----LMEKEKLCIKIITQIREMLEKDSVVEGNTIARKILN 1701
QY 296 -----GLGLTLPANONGIAHLAKSSNFYAOLSQQDAKASE 331
DB 1702 RYFKGDYSIGV-----NG--HLSGAVSKTAQVGVSGSDSD 1736

RESULT 12
DIMH_CAEEL STANDARD; PRT; 525 AA.
ID DIMH_CAEEL 017397;
AC 017397;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Diminuto-1-like protein.
GN F52H2.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peioderinae; Caenorhabditis.
NCBI_TaxID=6239;


```

RC STRAIN=RSY255;
RA MEDLINE=95014199; PubMed=7929113;
RA Duden R., Hosobuchi M., Hamamoto S., Winey M., Byers B., Schekman R.;
RT "Yeast beta- and beta'-coat proteins (COP). Two coatomer subunits
RT essential for endoplasmic reticulum-to-Golgi protein traffic.";
RL J. Biol. Chem. 269:24486-24495(1994).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=96437978; PubMed=8840506;
RA Bacciaro V., Eraso P., Portillo F., Mazon M.J.;
RT "Sequence analysis of a 14.6 kb DNA fragment of Saccharomyces
RT cerevisiae chromosome VII reveals SEC27, SSM1b, a putative
RT S-adenosylmethionine-dependent enzyme and six new open reading
RT frames.";
RL Yeast 12:887-892(1996).
RL [3]
RP SEQUENCE OF 1-27.
RC STRAIN=BJ926;
RX MEDLINE=94009692; PubMed=8405452;
RA Harter C., Draken E., Lottspeich F., Wieland F.T.;
RT "Yeast coatomer contains a subunit homologous to mammalian
RT beta'-COP.";
RL FEBS Lett. 332:71-73(1993).
CC -1- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS
CC TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-
CC CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC
CC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI
CC NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUNDLING FROM GOLGI
CC MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER
CC TRANSPORT OF DILYSINE-TAGGED PROTEINS.
CC -1- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,
CC BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.
CC -1- SUBCELLULAR LOCATION: THE COATOMER IS CYTOSOLIC OR POLYMERIZED
CC ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE
CC VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U11237; AAA61711.1; -
DR EMBL: X92670; CAA63359.1; -
DR EMBL: Z72659; CAA96848.1; -
DR SGSD; S0003105; SEC27.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 6.
DR PRINTS; PR00320; GPROTEINERPT.
DR ProDom; PD000018; WD40; 3.
DR SMART; SM00320; WD40; 6.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS50082; WD_REPEATS_2; 5.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
DR Transport; Protein transport; Golgi stack; Membrane; Repeat;
KW WD repeat; Endoplasmic reticulum.
FT REPEAT 11 41 WD 1.
FT REPEAT 53 83 WD 2.
FT REPEAT 95 125 WD 3.
FT REPEAT 138 169 WD 4.
FT REPEAT 182 214 WD 5.
FT REPEAT 226 256 WD 6.
SQ SEQUENCE 889 AA; 99444 MW; 6A5E50BBEB02CB58 CRC64;
Query Match 5.4%; Score 96.5; DB 1; Length 889;
Best Local Similarity 19.8%; Pred. No. 36;
Matches 65; Conservative 56; Mismatches 127; Indels 79; Gaps 14;
QY 19 WNEGNENKVLINLIKVLPTQVSGYNIEYTEPDCYSDASIQ--SLPDVFSTDSIFLPYLVS 77

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Db 476 WSDNGELWMTVNTNSN--GDEASGYTLLENK-DALYLEAANNINIDSEGVDEAF----- 526
QY 78 IGGVKSILDESIVRGV-TGDLHSFVSSASVYV-----GSVGFPOYLCNFFLSSPNGTQOA 132
Db 527 -DVLYELSESITSGKNMGVDVFFITTAIYNLNFVGGKTYVLAHYTKMYLL-----GYLAR 581
QY 133 SLLELAQK---VGYEQIYPDVASSSFTVFGLYVQQLQ-----SSSAADV1 178
Db 582 DNKMYLADREVHVVGYE--ISLVLPEQTLTLRGEIEEALENVLPNVEKDSLTKIARFL 639
QY 179 KASDLPQSGQVQVKDITQKRTILDSIVVASQREYINSVQKPKISNYVYGSESMEIK 238
Db 640 EGGYVEEALNISPDQDFELAL-----KVQ-----LTLAR 672
QY 239 DIIRDQVYNQILIGTSDPKPVYTVLALNSNLCDKQKAVAEVYKNLITNLTVDLGLG 298
Db 673 DLITDESAEMKWRALGD-----ASLGRFNKLAVEA-----FTVAHDLSEJFL 716
QY 299 LTLPAKNGIAHLAKSSNFFYALQSQFPA 327
Db 717 HSSFNNKEGLVTLLAKDERAKFNLAFA 745
RESULT 15
ID Y045 MYCPN STANDARD; PRT; 485 AA.
AC P75056;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipidprotein MG045 homolog precursor (D09_Orf485).
GN MG058 OR MG096.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_Taxid=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., La B.-C.,
RA Hermann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE000011; AAB95744.1; -
DR InterPro; IPR000044; Lipopr MG045.
DR Pfam; PF02030; Lipoprotein_8; 1.
DR PRINTS; PR00905; MYCMG045.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Hypothetical protein; Lipoprotein; Membrane; Signal;
KW Complete proteome.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 485 HYPOTHETICAL LIPOPROTEIN MG045 HOMOLOG.
FT LIPID 23 23 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 485 AA; 55019 MW; 1AD4E0AB211B64F8 CRC64;
Query Match 5.3%; Score 96; DB 1; Length 485;
Best Local Similarity 21.8%; Pred. No. 16;
Matches 61; Conservative 47; Mismatches 116; Indels 56; Gaps 13;
QY 24 NEVKLNLIRKDVLPQVSGYNIEY--TEPDCYSDASIQ--SLPDVF--STDSIFLPYLVS 77

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Db      201 HEVK-NTYDVNPT---GSTLNYFGVNYESFANLGLKRDNLTLFVNSDSNIIINELAN 255
Qy      78  ---LGWKSJDESIVRGVTDGLHSHFVSSASVNGSVYGFQYLCSNPLSSPNGTQOASS 134
Db      256 GRROGGIVYNGDAVYAAIGDLDREINENNL PNG-----DNFHIYQPKHSPVALD 305
Qy      135 LLELAQKVGEQIVYPVASSSFTVFGLYOQLLOSSSSAAVDIKASDLPQSGDVNKKDI 194
Db      306 FLINQ---QTHFRDAA-----HQLIYQALBEGADQTAEBELKTDEKGTSD 350
Qy      195 TOKRTILDSTVVASQR-EYINSVKQKPKISNYVGY--SESMCEIKDIIRDQYVQL 250
Db      351 EDYY-----TYGAMQNFSSVYVYVSPLNKINISDETTGIVFKENKQADTKQVVKQOSQSEQ 404
Qy      251 IGTSKDP-----YVTDVLAJNSNLCDEKQKVAVEYIK 283
Db      405 SESAKEETEODDFTYATLKSLKADSLDDKAKKLVDTIK 444

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Session completed: January 24, 2003, 19:41:59
 Job time: 18 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 24, 2003, 19:40:35 ; Search time 22 Seconds

(without alignments)
1555.630 Million cell updates/sec

Title: US-09-675-509-4

Perfect score: 1802

Sequence: 1 MSTRQKTLTVGLFPPYLSMN.....CVDPAKKEVKNAGVLRPPL 356

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR_73:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	230	12.8	409	2 T47118	thiamine pyridinyl
2	116	6.4	1248	2 B96827	hypothetical prote
3	115.5	6.4	886	2 S73184	phycobillosome link
4	111.5	6.2	613	2 B90294	hypothetical prote
5	111.5	6.2	2670	2 T37919	GCN1 homolog - fis
6	109	6.0	448	2 T06799	fimbria/plastin-11
7	108.5	6.0	998	2 T32787	hypothetical prote
8	108	6.0	528	2 T22583	hypothetical prote
9	108	6.0	885	2 S20621	phycobillosome anch
10	106.5	5.9	1033	2 A96714	hypothetical prote
11	106.5	5.9	2819	2 A90551	conserved hypochet
12	106	5.9	545	2 D75208	sugar abc transpor
13	106	5.9	1054	2 G82934	hypothetical prote
14	105.5	5.9	358	2 AB1746	hypothetical prote
15	105.5	5.9	1277	2 E70224	hypothetical prote
16	104.5	5.8	512	2 S06115	benzoylformate dec
17	104.5	5.8	512	2 S06115	alpha-amylose (EC
18	104.5	5.8	628	2 A82889	hypothetical prote
19	103.5	5.7	512	2 S23355	alpha-amylose (EC
20	103.5	5.7	682	2 G90284	hypothetical prote
21	103	5.7	286	2 A8665	outer membrane lip
22	103	5.7	637	2 AH1519	hypothetical prote
23	102.5	5.7	685	2 G69864	penicillin-binding
24	101.5	5.6	728	2 D86278	hypothetical prote
25	101.5	5.6	831	2 F90294	hypothetical prote
26	101.5	5.6	1787	2 AG1360	probable tape-meas
27	101.5	5.6	1787	2 D97316	probable S-layer p
28	101.5	5.6	2401	2 T28676	thoptry protein -

30	101	5.6	1042	2 H70203	isooleucine-tRNA 11
31	100.5	5.6	745	2 E64559	outer membrane pro
32	100.5	5.6	937	2 B86210	protein F22G5.6 [1
33	100	5.5	433	2 S77508	sera protein - Syn
34	100	5.5	672	2 D81746	type III secretion
35	99.5	5.5	701	2 S62460	hypothetical prote
36	99	5.5	507	2 S33921	alpha-amylose (EC
37	99	5.5	566	2 F70028	transmembrane rece
38	99	5.5	889	2 T45691	receptor-like prot
39	99	5.5	1159	2 S22768	130K protein - mal
40	99	5.5	1657	2 T25421	hypothetical prote
41	98.5	5.5	1160	2 I40589	transportal crystal
42	98.5	5.5	1161	2 E86626	transcription-repa
43	98.5	5.5	1308	2 A90428	serine proteinase,
44	98	5.4	389	2 H90083	polyadenylate-bind
45	98	5.4	429	2 A81315	probable MCP-type

ALIGNMENTS

RESULT 1

T47118

thiamine pyridinylase (EC 2.5.1.2) precursor [validated] - Paenibacillus thiaminolyticus

N:Alternate names: pyrimidine transferase; thiaminase I

C:Species: Paenibacillus thiaminolyticus

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 03-Jun-2002

C/Accession: T47118

R/Costello, C.A., Kelleher, N.L., Abe, M., McLaflerty, F.W., Begley, T.P.

J. Biol. Chem. 271, 3445-3452, 1996

A>Title: Mechanistic studies on thiaminase I: overexpression and identification of the

A/Reference number: 224363; PMID:96216437; PMID:8631946

A/Accession: T47118

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-409 <COS>

A/Cross-references: EMBL:U1768; NID:9984284; PIDN:AA04156.1; PID:9833806

A/Experimental source: strain 168

C/Function: monomer [validated, PMID:96216437]

A/Description: EC 2.5.1.2 [validated, PMID:96216437]

C/Keywords: transferase

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-409/Product: thiamin pyridinylase #status predicted <MAT>

Query Match 12.8%; Score 230; DB 2; Length 409;

Best Local Similarity 25.2%; Pred. No. 1.1e-08;

Matches 90; Conservative 53; Mismatches 146; Indels 68; Gaps 14;

Query 7 TLTAVGLPPYLPSPNNGENGVKILNKDVLPTQVSGVNIETFPDCYSASLSQSLPVPFS 66

Db 40 TLKVAIIPYVP-----DPAKFOAAVLDQKQROEPGVKLFETMDYSADPPDL-DVFFV 92

Query 67 TDSIFLPYLVSLG----GVKSLDESLVRCVTDLSFVSSASVNGSVYFPQVLCNPF 121

Db 93 LDSIFLPSHFVADAGVLLPFGSDIDQA-----EDVLPFALQAKRNGEVGLQILCTNL 146

Query 122 LSSPMTQ--QASSLLEAQKVG---YEQIVRPD-----VASSSFTYVGLYQQLQSS 171

Db 147 LFKRKGLKIGQVDNIVELYKKIGTSHSEQIPPOKMGILLINNAAGTTKASWYLE----- 201

Query 172 SSAAVDIKAS-----LPQSDQVNDKIDTKVYRTILST-----VVAASREYINSXKG 220

Db 202 --LIDVTGQYTYDILPLPDPLNDKVIKRLILINNAAGEKPSQVYRPGDDAVVRSWFA 259

Query 221 KPISSNYVYGSESMCEIKIIRDOQVNVQIGTS--DKPYVYTDVLAISNLCDKQKV 277

Db 260 QGSGRAPIGVSESMKMGDA--EQVRFKPISSAAGQDIPLPFSDVVSXKTAHP---- 313

Query 278 AVEYIKLTLNTLVLDLGLGL-----TLPAKKGKIHAKSSNFFYQQLSQ 323

Db 314 --ELAKKLANVMAADTVEQALRPQADGVQVYLLPRAHQVVEALMQDPYIVSELAQ 368

RESULT 2

hypothetical protein TRK14.1 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #ext_change 31-Mar-2001

C/Accession: B96827

R/Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Hughes, B.; Hinz, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maity, R.; Maritali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A86141; M01D:21016719; PMID:11130712

A/Accession: B96827

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1248 <STO>

A/Cross-references: GB:AE005173; NID:g4835752; PIDN:AA030219.1; GSPDB:GN00141

C/Genetics:

A/Gene: TRK14.1

A/Map position: 1

Query Match 6.4%; Score 116; DB 2; Length 1248;

Best Local Similarity 19.1%; Pred. No. 6.7; Mismatches 123; Indels 126; Gaps 17;

Matches 75; Conservative 69; Mismatches 123; Indels 126; Gaps 17;

14 PYLPSW-----NENGENEYKILN-----LIKD-VLPQVS-----41

26 PFMFDQGSASAMRPNNSGSDVKAHANPSIQGEFSLFPMDDRYIPQSSNPNGAGD 85

42 -GYNIEYTER-----DCYSDASLOS-----LPDVSTDSIFLPYLVSLGYSKL 84

86 MNVYTGMEIRGLIGISHTGSECDVSRFSTVENGTSDIERTNSLHEFNKLNHVQSA 145

85 DESLYR--GVYGDHAFSSSSASVNGSVYGFQYLCS--NFLSSPNTQ-----QASSL 135

146 PQALLSKDSSVGNLHGKYNSSASGSVTAKIKLCSFGKILPRPGDSKILRYVGGEHTI 205

136 LELAKQYBQI-----VYPDVASSSFTVFGLYQ-----QLQSSSSAAVDIKASD- 182

206 ISIKDLSWGLRQKILEIY-----YQIRVYKQLPGEPLDLVSVSSSED 251

183 ----LPSGQDVNKDITQKRTIILDSIVASQREYINSVKQKPISNYYVGSSEMCERK 238

252 LQNNLEENEMENRGSGQKLMPLFS--ISDMDDLGVNKNDDGSEF-----297

239 DIIRDQYNVOLIGTSKRPYYTVDLAINSLCEKQKVAVEIKLNTLTVLDLGLG 298

298 ----GYVAVNMDIGSGKNSITLLGLDSSANNLALDVRNTEGI--NTIAGDVGVG 349

299 LTLPANKGIAHLAKSSNFYAQLSQDFPKASE 331

350 -----ASGLMNGFQQTSAQOSE 367

RESULT 3

phycoobilisome linker protein apce - red alga (Porphyra purpurea) chloroplast

C/Species: chloroplast Porphyra purpurea

C/Date: 19-Mar-1997 #sequence_revision 09-May-1997 #ext_change 10-Sep-1997

C/Accession: S73184

R/Reith, M.; Munholland, J.

Plant Mol. Biol. Rep. 13, 333-335, 1995

A/Title: Complete nucleotide sequence of the Porphyra purpurea chloroplast genome.

A/Reference number: S73108

A/Accession: S73184

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-886 <RET>

A/Cross-references: EMBL:U38604; NID:g1276652; PID:g1276729

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995

C/Genetics:

A/Gene: apce

A/Genome: chloroplast

C/Keywords: chloroplast

Query Match 6.4%; Score 115.5; DB 2; Length 886;

Best Local Similarity 20.5%; Pred. No. 4.3; Mismatches 124; Indels 109; Gaps 17;

Matches 75; Conservative 57; Mismatches 124; Indels 109; Gaps 17;

54 SDASLOSPLDVSTDSIFLPYLVSLG-GYKSLDESIVRGVTGL-----HSFVS--SS 103

521 SSANFENSVDVIAKVS-----YLRVFGREYQGEKLLRPIESQLQDQGISVREFIQLAK 576

104 ASVNGSVYGFQYLCS-----NFLSSPN-GTQOASSLLEAKQYGEQIYPDVASSS 156

577 SSIFRSLYWEPLTYCAIEYIHNRLGRPYGQEIINKYFDIYKGYGVVDAILDSPE 636

157 SFTVFG-----LYOQLQSSSSAAVDI-KASDLPQSGD 188

637 YITFGENVYPRERYTTPAGIALRSIRPGIIDQRFKVISSKSRFVGLGKVEIRSN 696

189 -----ONKDIQKRTIILDSIVASQREY--INSVQKRPISN 225

697 IQSRIAGVTALRDQGVTFPDNQNSSQE--VLEQALRAAYRQIFERDLNFSIGEF 753

226 YVYGYSSEMCETDIIRD-----QQY--NQQLIGTSQK-----PYYTVDLAL 266

754 IESSFLNKQIVNKELOKALSELGYKEFYQYPNTKIVELGTRKHLIGRAPNNQAEIRFL 813

267 NSNLCEKQKVAVEIVIKNL-----TNTLVLDLGLGLTLPANKGIAHLAKSSNFYA 319

814 NQLASGLSTFETLVNNSSEYDSVYGTNTVPRRRP--TLPA-----ANFPTETLVN 865

320 QLSQ 324

866 RLTKQ 870

RESULT 4

hypothetical protein SSO1375 [imported] - Sulfolobus solfataricus

C/Species: Sulfolobus solfataricus

C/Date: 24-May-2001 #sequence_revision 24-May-2001 #ext_change 24-May-2001

C/Accession: B90294

R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,

arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A/Description: Sulfolobus solfataricus complete genome.

A/Reference number: A99139

A/Accession: B90294

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-613 <KUR>

A/Cross-references: GB:AE006641; NID:g13814587; PIDN:AAK1609.1; GSPDB:GN00155

C/Genetics:

A/Gene: SSO1375

Query Match 6.2%; Score 111.5; DB 2; Length 613;

Best Local Similarity 19.5%; Pred. No. 4.7; Mismatches 113; Indels 165; Gaps 22;

Matches 85; Conservative 72; Mismatches 113; Indels 165; Gaps 22;

13 FPY---LPSNENG-----NEVKILNL-IKDVLPQVSGYN-----44

88 YPVNQVWVFNYPENGLPLNMSYDNMSIHEISFIALPTVDVYPTKI--YNSSLYLKGLLS 145

45 -----LEYTEPCYSDASQSLPD--VFSTDSIFLPYLVSLGCV-----KSIDES 87

146 ATYKNAIIIIISYDKFSKY-NITLSQYPSHILQGTGIGL-FIIPDLQALPWVYKSVNS 203

QY 88 LVR-----GVTGDLHSFVSSASVN-GSVYGPQYLCNFL 122
 Db 204 VIOQYIFONETNLTINGNDFSLTQGLYDELSTVOTLEFLNTTSPY-----SSIL 256
 QY 123 LSPNGTQOA-----SSLLELA-----QKVGEOY----- 148
 Db 257 IDSJNNTTEAMANRPITDNTDINSIIDLAYSSSTLTPGEOEFAYIYFSGNITTKIES 316
 QY 149 -----YPDVASSSFVFGLYOQLLOSSSSAANDIKASDLPQSGDQVNDKI 194
 Db 317 EIVELPLVNLVIOYPSISNOSPITIVFVNLNRSATKVEGVYGLYNSTG----- 369
 QY 195 TOKRTITDSTVVASQREYINSVKQKPISNY-----VGYSESMCEIKDIIRD--QOY 246
 Db 370 -----LISKISMNSNGELVFNVSPGTIVLYVHYHPNLGLNTEYWGQIRIDVREGINKY 423
 QY 247 NVOLIGTSDEKRYVTVDLALNSNLCDEKQKAVEYIKULTNTLVLDLGLGLTIPANKN 306
 Db 424 NF-----TRVEPMYINII-----DTSIDSQFKISVKLIINPL--NQTVSGQLYIMIS-----N 468
 C 307 GIAHLAKSNFYAOL 321
 Db 469 GIASSASAPTESOL 483

RESULT 5

T37919
 GCNI homolog - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
 C:Accession: T37919
 R:Conor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.
 submitted to the EMBL Data Library, December 1995
 A:Reference number: Z21754
 A:Accession: T37919
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-2670 <CON>
 A:Cross-references: EMBL:Z68198; PIDN:CAA92385.1; GSPDB:GN00066; SPDB:SPAC1866.05C
 A:Experimental source: strain 972h-; cosmid c1866
 A:Gene: SPDB:SPAC1866.05C
 A:Map position: 1
 A:Introns: 50/1

Query Match 6.2%; Score 111.5; DB 2; Length 2670;
 Best Local Similarity 19.7%; Pred. No. 45;
 Matches 77; Conservative 60; Mismatches 146; Indels 107; Gaps 17;
 C 10 VGLF--PYLP-----SMNNGNEVKLINL-----IDVLP.TOVSGYNI 45
 Db 1433 LGIYFEPYLPDLLPULLTSGFDNANEVREATMDAVKQIMSQSASGVALLPTLLDGLN- 1491
 QY 46 EYTFEDCYSDASLOSPLPVFSTD--SIFLPYLVSLGVKSIDESIVRGVTDGLHSFVSS 103
 Db 1492 EYNNRSKASAVEILGLMSYMAPKQSLVPLPTI-----IPKLSVLT-----DSHQVANT 1541
 QY 104 ASVN-----GSVYGF--OYLCNPLSSPNGTQOASSILELAQKVGQIYIPV----- 152
 Db 1542 ANKSLRFGDVISNPEIQTLPVLLKALSDCTRYDADLEALLKTSFVHYLDPPSLALVI 1601
 QY 153 -----ASSSFYFGLYOQLLOSSSSAAV-----DIKASD 182
 Db 1602 PILKYLGRNAGTKRGQAKIFGLMASTLTPENLAVYIESLMPRLREVLIDPVPTRATA 1661
 QY 183 LPQSGDQVNDKITOKYRTILDS--TVVASQREYINSVKQKPISNYVYVYGESMCE--IK 238
 Db 1662 AKALGSLIEKLEKKFPLIEPLFVNLRSCEGEVDRQGAQGLSITLGLGLARLEVDLP 1721
 QY 239 DIIRDQ-----YVQLIGTSDEKRYVTVDLALNSNLCDEK---QKAVE 280
 Db 1722 EILKNTSSPVPHIREPISLILYLPATGSRFPQYLABAIPILPISGLADSELVGTASLR 1781

QY 281 VIKNLTN--TLVLDLGLGLTIPANKGI 308
 Db 1782 AAKMIVNNVATKSVDLL-----LPELEKL 1806

RESULT 6

T06799
 fimbrin/plastin-like protein - wheat (fragment)
 C:Species: Triticum aestivum (common wheat)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
 C:Accession: T06799
 R:Crüz-Ortega, R.; Cushman, J.C.; Ombry, J.D.
 Plant Physiol. 114, 1453-1460, 1997
 A:Title: cDNA clones encoding 1,3-beta-glucanase and a fimbrin-like cytoskeletal protei
 A:Reference number: Z15824; MUID:97422889; PMID:9276954
 A:Accession: T06799
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-448 <CRU>
 A:Cross-references: EMBL:U67717; NID:G1575594; PIDN:AA049813.1; PID:G1575595
 A:Experimental source: cv. Victory; root; 4 days old
 C:Function:
 A:Description: actin-bundling
 C:Superfamily: plastin; alpha-actinin actin-binding domain homology; calmodulin repeat
 C:Keywords: actin binding; EF hand

Query Match 6.0%; Score 109; DB 2; Length 448;
 Best Local Similarity 20.7%; Pred. No. 4.4; 155; Indels 68; Gaps 17;
 Matches 77; Conservative 72; Mismatches 17;

QY 16 LPSNNGNEVKLINLKD-----LPTOVSGYNIETEPDCYSASLQS 60
 Db 5 LNPBERNHTLCLNSAKAIGCTVNIQTQFLVGRPHVLVGLISQIKIQLADLNLKK 64
 QY 61 LPDVFS--TDSIFLPYLVSLGVKSLDESIVR-----GVTGDLHSFVSSASVNGS 109
 Db 65 TPQVLELPDSDKIDVLSL-----STEKMLRWNNHHLKKAQYKKTNNF--SSDVADGE 118
 QY 110 VYGF-----POYLCNPLSSPNGTQOASSILELAQKVGEOIYVP-DVASSSFYVFG 162
 Db 119 AYAVLLAALAE-TSPETLETKNPDERAKKVLQAEKLDCKRYLTPKDIETESSANLNA 177
 QY 163 LYQQLQSSSSAAVDIKASDLPQSGDQVNDKITOK---YRTITDSTVVASQREYINSVKQ 219
 Db 178 FVAQIFQHRNGLTSDIQVLTQTSASRDVLSNEERAFPMWINSLGES---YLNVFE 234
 QY 220 GKPISNYVYVYGESMCEIKDIIRDQVNVOLIGTSDEKPYVTVDLALNSNLCDEKQYAV 279
 Db 235 --DVNRGMV-----LLEVLDKVSFGSVNMWL--ESKRPILKPRKLEN--CNOVVIGK 282
 QY 280 EV---INKLNTNLVL--DLGLGLTIPANKGIHLAKSNFYAOLSQOPDAKESEVRV 334
 Db 283 ELKPSLVNLAGNDIVQGNKKLIVALLWQLMKPFNLQLNLRSHRSKSGSQGQITDADI-- 340
 QY 335 LRCVDFANKEVK 346
 Db 341 ---LNMANSKVK 349

RESULT 7

T32787
 hypothetical protein F14D2.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T32787
 R:Du, Z.; Ye, T.T.
 submitted to the EMBL Data Library, December 1997
 A:Description: The sequence of C. elegans cosmid F14D2.
 A:Reference number: Z21225
 A:Accession: T32787
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-998 <DUZ>

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A96714

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1033 <STO>
A:Cross-references: GB:AE005173; NID:g6358765; PIDN:AAF07347.1; GSPDB:GN00141
C:Genetics:
A:Gene: T6L1.12
A:Map position: 1

Query Match 5.9%; Score 106.5; DB 2; Length 1033;
Best Local Similarity 20.6%; Pred. No. 24;
Matches 96; Conservative 73; Mismatches 135; Indels 163; Gaps 26;

QY 1 MSTOPKTLTVGLFPYLPSPWNGNEVKLIN-----LIRDLVPTQVSG 42
D 85 LSNMQUANTIG-----DGSKEMINNGQOKISAKHTPDIVSEGMEDLVPTDP-- 132
QY 43 YNIYTEPDCSDASLQ--SLPDV--FSTDSIFLEPLVS---LGSVSLDSLVKGTGD 95
D 133 -EFSYESYMYSESOSQWTDIPDIPSKSTD-----VSROKIGNHSESQSLVTEIP-D 183
QY 96 L-----HSFVSSASVNGSVYGFPOYLCNLFLLSPNGTQO-----ASSLLE 137
D 184 IPSQSTVSSQKRGKNSKSSQSQSTETIPDIPS-----QSSNASQKRYGNLSSESLSM 235
QY 138 LAQ-----KVGVEQIVYPDVASSSFTVFGLYQQLLOSSSAVAVDIKAS-----DLP 184
D 236 LPQVTOGMEPPYQAFIC-----LTKEIMEDPVTTGCVTCERQAVIEWPDSF 283
QY 185 QSGQOVNKDIT-QYRTITLDSVVASQREYNSVKQKPISN-----YVGYSE 232
D 284 GNSDEINCPVYQKLTTELISANVV-----LKTIIQEWKVENHAKIKVAHAALSLGSE 337
QY 233 SMCEIKIIRP-----QQVN-----VOLIGTSDKRYVVT-----DVLALNSNL 270
D 338 SM--VIDLRLQMTCEGKEYNKQVREAGITQLL--DRYLTVRSKQVRELLKFLRTL 392
QY 271 CDEKQKAVEYIKNLTFTLVLDLIG-----LGLTPPANKN-----GIALHAK 313
D 393 ADEETDCKEIVITITMSCYIKLLGSSHOVRHAQKLLLELSQACKEKIGTARAI 452
QY 314 SSNFYAQLSQQFD--AKSESEVRVLRCVDPANKEVNKA--GVLRPFL 356
D 453 LMLVTAKYNRELDSFASSETSDOILRNLEKCPENIKOMAESGLLEPLL 499

RESULT 11
A90551
conserved hypothetical protein MYPU_3130 [imported] - Mycoplasma pulmonis (strain UAB CT

C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: A90551
R:Chamand, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen *Mycoplasma pulm*
A:Reference number: A95512; MUID:21267165; PMID:11353084
A:Accession: A90551

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2819 <KUR>
A:Cross-references: GB:AL445566; PID:G14089727; PIDN:CAC13486.1; GSPDB:GN00153
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU_3130
A:Genetic code: SGCS

Query Match 5.9%; Score 106.5; DB 2; Length 2819;
Best Local Similarity 20.8%; Pred. No. 1.1e+02;

Matches 77; Conservative 66; Mismatches 105; Indels 123; Gaps 19;

QY 25 EVKILNLIKDLPTQVSGYNIETEPFCYSDASLQSPDVSTDSIFLPLVSLGKVS 84
D 1358 EIKSSNIITQRLGGTIALVTNPG--KIFSDTELQSLSTLIN-----ESL 1401
QY 85 DESLVRGVTDLHSPVSSASVNGSVYGFPOYLCNLFLLSPNGTQOASSLLEAKQVY 144
D 1402 DLFKNTIINSLYDLVLSALISIN-----QSSSVL---TKV-- 1434
QY 145 EQIYPPVASSSFTVFGLYQQLLOSSSAVAVDIKASDLPQSGQVKNKITQKRTILDS 204
D 1435 ENITHKALDOQNSY--FAVIKTLL-----SVKEDVDVKSDE--FKAIKKFLNLF-- 1480
QY 205 TVVASQREYNSVKQKPISNVYGY-----SESMECEIKIIRPOQ---YVVOIGT--- 253
D 1481 ---AKNDYL-LTKFISPIDKTIIDFDSATKSSIVKLIKVLSEQLKRSQAQIITDITFA 1535

QY 254 -SDKPYVY-----TDVLALNSNL-----CDEKQKVAVE--VIRKILT--- 287
D 1536 NKNKYLAIVENLDFLDALVDNKENIINLSNTLGKIKTDEFPKNIITKSFITKXLMTSDS 1595

QY 288 -----NTVLVDLGLTLPPANKNGIAHLAASSNFYAQLSQQFDA-----KESEYRV 334
D 1596 SITEEETNTIV-----KSAHELISIVDSNLFNLQKLFALLLEKMKKDSKSTS 1644
QY 335 LRCVDPANKEV 345
D 1645 LEFSTFMKKSI 1655

RESULT 12

D75208
sugar abc transporter binding protein related PAB2439 - Pyrococcus abyssi (strain Orsay
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: D75208
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A:Reference number: A75001
A:Accession: D75208

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-545 <RAM>
A:Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49115.1; PID:g54576.
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2439

Query Match 5.9%; Score 106; DB 2; Length 545;
Best Local Similarity 25.0%; Pred. No. 9.7;
Matches 38; Conservative 24; Mismatches 68; Indels 22; Gaps 6;

QY 19 WNEGNEVKILNLIKDLPTQVSGYNIETEPFCYSDASLQSPDVSTDSIFLPLVSL 78
D 92 WKENGIVNKIV-IPEDMIRYDQS--FKDYQDEF--LSKQPLQAGADFPVNSAFLPNLAEE 147
QY 79 GGVVSLDE--SLVRYGTGDLHSPVSSASVNGSVYGFPOYLCNLFLLSPNGTQOASSL 136
D 148 GYILIDITDYAKAVGSVNDPFPSLLEAKYKGRLYGAPQ-----DREARPLY 194
QY 137 ---ELAQKVGVEQIVYPDVASSSFTVFGLYQ 165
D 195 IRKDVACVGLDVSTLDPDKVNGEFTWSDYVE 226

RESULT 13

G82934
hypothetical protein U0094 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: G82934

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 24, 2003, 19:41:50 ; Search time 12 Seconds
(without alignments)
598.630 Million cell updates/sec

Title: US-09-675-509-4

Perfect score: 1802
Sequence: 1 MSTOPKTLTVGLPFLPSMN.....CVDFAKVKNCAGVLRLPL 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 122226 segs, 20178551 residues

number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:
1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB pep.*
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11: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.5	5.6	745	8 US-08-834-666A-6	Sequence 6, Appl
2	97.5	5.4	2037	10 US-09-951-402-3	Sequence 3, Appl
3	97.5	5.4	2037	10 US-09-951-401-3	Sequence 3, Appl
4	97.5	5.4	2037	10 US-09-922-101-3	Sequence 3, Appl
5	97	5.4	615	9 US-09-992-598-194	Sequence 194, App
6	97	5.4	615	9 US-09-989-293A-194	Sequence 194, App
7	97	5.4	615	9 US-09-989-735-194	Sequence 194, App
8	97	5.4	615	9 US-09-990-444-194	Sequence 194, App
9	97	5.4	615	9 US-09-989-730-194	Sequence 194, App
10	97	5.4	615	9 US-09-980-436-194	Sequence 194, App
11	97	5.4	615	9 US-09-991-181-194	Sequence 194, App
12	97	5.4	615	9 US-09-993-687-194	Sequence 194, App
13	97	5.4	615	9 US-09-989-734-194	Sequence 194, App
14	97	5.4	615	9 US-09-997-653-194	Sequence 194, App
15	97	5.4	615	10 US-09-989-723-194	Sequence 194, App
16	97	5.4	615	10 US-09-989-723-194	Sequence 194, App
17	97	5.4	615	10 US-09-989-729-194	Sequence 194, App
18	97	5.4	615	10 US-09-989-727-194	Sequence 194, App
19	97	5.4	615	10 US-09-989-731-194	Sequence 194, App

20	97	5.4	615	10 US-09-989-732-194	Sequence 194, App
21	97	5.4	615	10 US-09-991-073-194	Sequence 194, App
22	97	5.4	615	10 US-09-990-442-194	Sequence 194, App
23	97	5.4	615	10 US-09-991-163-194	Sequence 194, App
24	97	5.4	615	10 US-09-993-604-194	Sequence 194, App
25	97	5.4	615	10 US-09-990-456-194	Sequence 194, App
26	97	5.4	615	10 US-09-989-721-194	Sequence 194, App
27	94.5	5.2	652	8 US-08-834-666A-16	Sequence 16, Appl
28	93.5	5.2	418	10 US-09-925-302-565	Sequence 565, App
29	93.5	5.2	991	10 US-09-815-242-5803	Sequence 5803, App
30	93	5.2	346	10 US-09-741-669-380	Sequence 380, App
31	92.5	5.1	592	9 US-10-027-806-80	Sequence 80, Appl
32	92.5	5.1	592	9 US-10-034-623-80	Sequence 80, Appl
33	92.5	5.1	607	9 US-10-072-436-11	Sequence 11, Appl
34	92.5	5.1	116	10 US-09-815-242-11849	Sequence 11849, A
35	92	5.1	468	10 US-09-765-272-10	Sequence 10, Appl
36	91.5	5.1	376	10 US-09-801-368-206	Sequence 206, Appl
37	91.5	5.1	722	10 US-09-815-242-12888	Sequence 12888, A
38	91	5.0	424	9 US-09-738-626-4306	Sequence 4306, Ap
39	90	5.0	2437	10 US-09-815-242-5834	Sequence 5834, Ap
40	90	5.0	6281	10 US-09-815-242-12996	Sequence 12996, A
41	89.5	5.0	384	9 US-09-738-626-4937	Sequence 4937, Ap
42	89.5	5.0	886	10 US-09-801-368-180	Sequence 180, Appl
43	89.5	5.0	963	9 US-09-764-868-877	Sequence 877, App
44	88.5	4.9	4563	9 US-09-870-759-128	Sequence 128, App
45	88	4.9	511	10 US-09-815-242-13865	Sequence 13865, A

ALIGNMENTS

RESULT 1
US-08-834-666A-6
; Sequence 6, Application US/08834666A
; Patent No. US20020044949A1
; GENERAL INFORMATION:
; APPLICANT: Kleantous, Harold
; APPLICANT: Liessolo, Ling
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Miller, Charles
; APPLICANT: Al-Garawi, Amal
; TITLE OF INVENTION: 76 Kda Helicobacter Polypeptides and
; TITLE OF INVENTION: Corresponding Polynucleotide Molecules
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESS: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: PASTESQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,666A
; FILING DATE: 01-APR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,175
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: 1...20
; OTHER INFORMATION:
US-08-834-666A-6
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Query Match          5.6%; Score 100.5; DB 8; Length 745;
Best Local Similarity 21.1%; Pred. No. 1.6;
Matches 63; Conservative 43; Mismatches 112; Indels 81; Gaps 11;
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QY 103 SAVNGSVYGFPPQYLCSNFFLLSPNG----- 128
D 212 TADINGGVYQCK--AKNGSSSSSSNGGSSSTQTATTGTODGVITTTNNKATVFKPD 269
QY 129 TQQAASSLLELAQKVGIEIV--YPDVASSSSFTVFGIYQQLQSSSAVDYKASDLPQ 185
D 270 TNNAEQLLNQANI--MQVLTQCPYVSTNNENTPGGGQPGWGLSTSGNAGSI----FQQ 323
QY 186 SGDOVNKDITQKRYTILDSITVVASGREYINSVKQKXPISNYV-VGYSRSGEIKDIIIRDQ 244
D 324 EFSQVTSMTKAQELIAQSKI VSENAQNNNDTGKPPNPPTDASFQSM-----LNKA 377
QY 245 QYNVOLIGTSKPYVYTDVLAALNSNLCDE---KQYAVEVIXKL----- 286
D 378 QAQEMFNLSPQVKKNLSEVMNNNNVNEKLAGFKEEYMTNFWFAFLASCCKDGLTPVAG 437
QY 287 --TNTVLVDLIGLITLTPANKNGIAHLAKSSNFYAQLSQQFDKASEVRVRCVDPANKE 343
D 438 VTSNTWGACAYVGETISALTNISIAH-----FQTEQOIQQAENIADTL--VNFKSR 487
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RESULT 2

```

US-09-951-402-3
; Sequence 3, Application US/09951402
; Patent No. US20020168752A1
; GENERAL INFORMATION:
; APPLICANT: Bartel, Paul L.
; TITLE OF INVENTION: MSC2- An MMAC1 Interacting Protein
; FILE REFERENCE: MMSC2
; CURRENT APPLICATION NUMBER: US/09/951,402
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US 09/306,998
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 60/084,740
; PRIOR FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2037
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-951-402-3
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Query Match          5.4%; Score 97.5; DB 9; Length 2037;
Best Local Similarity 21.4%; Pred. No. 11;
Matches 75; Conservative 48; Mismatches 147; Indels 81; Gaps 15;
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QY 7 TLTVGLFPYLPBSMNGENVEKILNLIKDVLPYQVSGYNIETEPDYSASLQSLPVS 66
D 778 TVRIGVAKPLPLSPBEG---YVSAKED-----SFLYPPHSC--EAGGLADKP-LFR 822
QY 67 TDSIFLPYLVSLGKVSLSDESLVGVGTGDLHSFVSSASVNGSVYGFPPQYLCSNFFLLSP 126
D 823 ADLA-----LVGTNDADLVDES-----TFESPYPSPENDSISTQASLISHGSSCG 868
QY 127 NGTQAASSLLELAQKVGIEQIVPDVASSSSFTVFGIY-----QQLQSSSSAAVDI 178
D 869 DGLNVGSSLPSSPPK-----DVLENSCDPVLDMHSLSEELYTONLQRODENTPSV 919
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QY 179 KASDLPQSGQOVN-----KOITQKRYTILDSITVVASGREYINSVKQKXPISNYVGYSES 233
D 920 DISMGPASGFTINDYTPANAIEQYE--CENTIWTESHLPSEV-----IS 963
QY 234 MCEIKDIIIPQOVVQVLIGTSKPYVYTDVLAALNSNLCDEKQKAVEVIXKLITNTVLVD 293
D 964 SAEIPLSVLPDS-----AGKSEYILQSSSLACNAE-CWMLQNVSKSPER--TINIAGK 1014
QY 294 LIGLGLTLPANKNGIAHLAKSSNFYAQLSQQFDKASEVRVRCVDPANKE 344
D 1015 NSSLGMTVSNKQGLGMIVRSIIGHAIS-----RDRIRIAGDILSINER 1060
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RESULT 3

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US-09-951-401-3
; Sequence 3, Application US/09951401
; Patent No. US20020115104A1
; GENERAL INFORMATION:
; APPLICANT: Bartel, Paul L.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: MSC2- An MMAC1 Interacting Protein
; FILE REFERENCE: MMSC2
; CURRENT APPLICATION NUMBER: US/09/951,401
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US 09/306,998
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 60/084,740
; PRIOR FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2037
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-951-401-3
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Query Match          5.4%; Score 97.5; DB 10; Length 2037;
Best Local Similarity 21.4%; Pred. No. 11;
Matches 75; Conservative 48; Mismatches 147; Indels 81; Gaps 15;
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D 920 DISMGPASGFTINDYTPANAIEQYE--CENTIWTESHLPSEV-----IS 963
QY 234 MCEIKDIIIPQOVVQVLIGTSKPYVYTDVLAALNSNLCDEKQKAVEVIXKLITNTVLVD 293
D 964 SAEIPLSVLPDS-----AGKSEYILQSSSLACNAE-CWMLQNVSKSPER--TINIAGK 1014
QY 294 LIGLGLTLPANKNGIAHLAKSSNFYAQLSQQFDKASEVRVRCVDPANKE 344
D 1015 NSSLGMTVSNKQGLGMIVRSIIGHAIS-----RDRIRIAGDILSINER 1060
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RESULT 4

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US-09-922-101-3
; Sequence 3, Application US/09922101
; Patent No. US20020146711A1
; GENERAL INFORMATION:
; APPLICANT: Bartel, Paul L.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: MSC2- An MMAC1 Interacting Protein
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FILE REFERENCE: NMSC2
CURRENT APPLICATION NUMBER: US/09/922.101
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/306,998
PRIOR FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 2037
TYPE: PRT
ORGANISM: Homo sapiens
US-09-922-101-3

Query Match 5.4%; Score 97.5; DB 10; Length 2037;
Best Local Similarity 21.4%; Pred. No. 11;
Matches 75; Conservative 48; Mismatches 147; Indels 81; Gaps 15;

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QY 67 TDSIFLPYLVSLGKVKSLDESLVGVGTGDLHSPVSSASVNGSVYGFPOYLCSNPLSSP 126
D 823 ADLA-----LVGTNDADLVDS-----TFESPYPSPENDSYSTQASITSLHGSSCG 868
QY 127 NGTQOASSLLELAOKVGEQIVPVDVASSSFTVFGLY-----QQLSSSSAAVDI 178
D 869 DGLVNGSSLSPEPK-----DVIENSCDPVLDLHMSLELYTQWLROBENTPSV 919
QY 179 KASLPQSGDQV-----KDTQKRTILDSITVVAQREYINSVKQKPISNVYVSES 233
D 920 DISGPPASGFINDYTPANALIEQOYE--CENTIIVTESHLPSEV-----IS 963
QY 234 MCEIKDIIRDQVNVQLIGTSDKPYVYTDVLANSNLCDEKQXAVEYIKXLTNTLVLD 293
D 964 SAELPSVLPDS-----AGKSEYLLBSSSLACNAE-CVMLOVNSKSEFER--TINIAGK 1014
QY 294 LLAGLTLTPANKNGIAHLAKSSNFYAQLSQQPDAKSEFVRVLRCDVPAKKE 344
D 1015 NSSLGMTVSNKDGKGMIVRSIIHGGAIS-----RDGRIALGDCLISINEE 1060

RESULT 5
US-09-922-598-194
Sequence 194, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zheng, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
PRIOR FILING DATE: 2001-11-20
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PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090477

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P R I O R   A P P L I C A T I O N   N U M B E R :   60/091982
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Query Match          5.4%; Score 97; DB 9; Length 615;
Best Local Similarity 21.3%; Pred. No. 2.3;
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QY 237 IKDIIRPOQVYVQLI-STSDKPYVYT---DVLALNSNLCDKQKV---AVEYIKNLLTNT 289
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QY 340 FANKEVN-CAGVL 352
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RESULT 8
US-09-990-444-194
Sequence 194, Application US/09990444
Publication No. US20020193300A1

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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertschen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivay J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zheng, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 5.4%; Score 97; DB 9; Length 615;
Best Local Similarity 21.3%; Pred. No. 2.3;
Matches 54; Conservative 50; Mismatches 112; Indels 38; Gaps 10;

119 SNFLSSPNGQOASLLLEAOKYGEIYVPPDVASSSFVFGLYOQLLOSSSAVD-177
147 AGILVSNPAVQAMELEYVLKKVGCALVFPKQKTOY--YVWLKQICEVENADPGA-204
178 IKASDLPOSGDQVAKDITQKRYTLDSTVVA--SOREYVNSYKQKAPISNYVYSESACE-236
205 LKSGRLPDLTIVVDAPLPGTLLDEYVAGSTRQHLDQ-----YNOQPLS-253
237 IKDIIRDQYVQOLI-GTSKPYVYT--DVLALNSMLCDEKQV--AVEVINKLLTNT-289
254 CHDEI-----NIQFTSGTSGPKGATLSHYNIYVNSNLSGRLKLUHEKTPQRLMLPNP-308
290 LVLDLGLGLLPANKKCIATLAKSSNYAQLSQQFDKKEE-----VRLKQVVD-339
309 LYHCLGSSVAGTMCMLMYGATLILASPIFNKKALEAISREGTFLYGTPTMVFVILNPPD-368

OY 340 PANKEVN-CAGVL 352
Db 369 FSSYDISTMCGVIL 382

RESULT 9
US-09-989-730-194
Sequence 194, Application US/09989730
Publication No. US20020197674A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC69
CURRENT APPLICATION NUMBER: US/09/989,730
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/065311
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73	PRIOR APPLICATION NUMBER: 60/0902522

[illegible]

Query Match	5.4%	Score 97	DB 9	Length 615
Best Local Similarity	21.3%	Pred. No. 2.3		
Matches 54	Conservative 50	Mismatches 112	Indels 38	Gaps 10

Oy	119	SNFLLSPNGQOASSLLELAQKXGEGQIYYPDVAASSSFVEGLYGOLLQSSSAVD-	177
Dd	147	AGIIIVSNPAVOMELFETVLAKRGCALVPFKFOQR--YNVLQICEVENAOPGA	204
Oy	178	IKASDLPSGDQVKDITOKRYRIILDSITYA-SOREXYINSVKOOKPISNYYGYSBMCE	236
Dd	205	LKSRLPLPTTVIVSDAPLPFTLLDEEVVAAGSRGHLDLO-----YNQOFLS	253

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OY      237  IKDIIRDOYVNOI-LGRSDRPYYVT---DYVALNSNLCDEKQV---AVEVINGLLTNT 269
DB      254  CHDPL-----NIQFSGTGSPPKATLSHYIVVNSNINLGRLLKHEKTEPQQLMILPNP 308
OY      290  LVLDLGLGLTLTPANKNGIAHLAKSSNFEYQLSOQFPAKES-----VFLRCVD 339
DB      309  LYHCLGSVAGTMMCMVATGATILASPINGKKALEAISREKGTFLYGPTMFWDLNQP 366
OY      340  FANKEVKR-CAGVL 352
DB      369  FSSYDISTMCGGI 382

RESULT 10
US-09-990-436-194
Sequence 194, Application US/09990436
Publication No. US20020198148A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: KJavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC14
CURRENT APPLICATION NUMBER: US/09/990.436
PRIOR APPLICATION NUMBER: 2001-11-14
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE:	1998-06-18

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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 5.4%; Score 97; DB 9; Length 615;
Best Local Similarity 21.3%; Pred. No. 2.3;
Matches 54; Conservative 50; Mismatches 112; Indels 38; Gaps 10;

QY 119 SNFLSSPNQQAASLLLEAQKGYEDIVYPDVASSSFFVFGYQQLDSSSSAAND- 177
D 147 AGILTVSNPAPYQAMELELVKVKCKALVPKQFKTOY--YVNLKQICEVEVAQGA 204
QY 178 IKASDLPOSGDQVKNKDITQKRTILDSTVVA--SOREYINSVKQKGFISNYVYGSSEMC 236
D 205 LKSGRLDPLTVIVSDALPBTLLDEVAAGSTRQHLDQ-----YNQQLS 253
D 237 IKDIIRDQVNVQLI-GTSDKPYVYT---DVLALNSLCKDEKQV--AVEVINKLTLNT 289
D 254 CHDPI-----NIQFTSGTGSFKGATLSHYNI VNNNSNLGRLKMKHKTPEQLRMILPNP 308
QY 290 LVLDLLGLGLTPANKGIAHLAKSSNRYAQLSQQFDKKESE-----VRYLRQVD 339
D 309 LYHGLGVAGTMCIMYGATLLASPIFNKKALEAISREKGTLYGTPMFWILNPD 368
QY 340 FANKEVKN-CAGVL 352
D 369 FSSYDISTMCGSVI 382

RESULT 12
US-09-993-687-194
; Sequence 194, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC11
; CURRENT APPLICATION NUMBER: US/09/993.687
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 5.4%; Score 97; DB 9; length 615;
 Best Local Similarity 21.3%; Pred. No. 2.3; Mismatches 10;
 Matches 54; Conservative 50; Indels 38; Gaps 10;

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 DB 147 AGITLVSNPAPYQMELEYLKVGCALVPPKQFTQY--YVNLKQICEVENAQPGA 204
 QY 178 IKASDLFQSGDPQVNDITQKXRTITDSTVVA-SQREYINSVKQKPISNYYVGSQMSCE 236
 DB 205 LKSGRLPDLTTVSVDAPLPGTLLDEVAASTRQHLDQLQ-----YNGQFLS 253
 QY 237 IKDIIRDQYVQGLI-GTSDEKYVT--DYLAISNLCDEKQV--AVEVINLLTNT 289
 DB 254 CHDPI-----NIQTSQTSSPKGATLSHYNIWNNSNLSERLTHKTEQQLMILPNP 308
 QY 290 LVLDLGLGLTPANKRGIAHIAKSSNFYAQLSQQFPAKSE-----VRLACVD 339
 DB 309 LYHCLGSSVAGTMCMLGATLILASPLFNGKALDAISRGRGFLYGTPTMFWIDLINOPD 368
 QY 340 FANKEVKN-CAGVL 352
 DB 369 FSSYDISTMCGVI 382

RESULT 13
 US-09-989-734-194
 Sequence 194, Application US/09989734
 Publication No. US2003000531A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Baton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurley, Austin L.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Nadler, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730P1C64

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; PRIOR FILING DATE: 1998-07-09

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Query Match          5.4%; Score 97; DB 9; Length 615;
Best Local Similarity 21.3%; Pred. No. 2.3;
Matches 54; Conservative 50; Mismatches 112; Indels 38; Gaps 10;

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QY 178 IKASDLQSGGVNKKDTQKRTILDSTVVA--SQREYINSKQGGKPISNYVGSSESC 236
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QY 237 IKDIIHQQVNVQLI-GTSDKPYVYT--DVLALNSNLDKQKV--AVEVKNLTLNT 289
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DB 254 CHDPI-----NIQFTSGTSGSPKCATLSHYNIYVNSNLGERLKLHETPQOLRNILPNP 308
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QY 290 LVLDLGLGLTLPANKGIAHLAKSNFYAQLSQQFDKASE-----VRYLRCDV 339
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DB 309 LYNHCLGSVAGTMMCLMWGATLILASPIFNKGKALEAISREKGTFLYGTPTWFVDILNQPD 368
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; Publication No. US20030008297A1
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
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; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gettisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann

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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC38
; CURRENT APPLICATION NUMBER: US/09/997, 653
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10	PRIOR APPLICATION NUMBER: 60/090696
11	PRIOR FILING DATE: 1998-06-25
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25	PRIOR FILING DATE: 1998-07-02
26	PRIOR APPLICATION NUMBER: 60/091633
27	PRIOR FILING DATE: 1998-07-02
28	PRIOR APPLICATION NUMBER: 60/091978
29	PRIOR FILING DATE: 1998-07-07
30	PRIOR APPLICATION NUMBER: 60/091982
31	PRIOR FILING DATE: 1998-07-07
32	PRIOR APPLICATION NUMBER: 60/092182
33	PRIOR FILING DATE: 1998-07-09

Query Match	5.4%;	Score 97;	DB 9;	Length 615;
Best Local Similarity	21.3%;	Pred. No. 2.3;		
Matches	54;	Conservative	50;	Mismatches 112;
				Indels 38;
				Gaps 10

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Qy	178	IKASDLPQSDQVNNKDITQYRTILLDSVYA-SOREYINSVKOGKPISNTYYGSEMC	2336
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Qy	237	IKDIIRROQVNVOLI-GTSPDKPYVT--DLVALNSNLCEKOKV--AVEVIKNLLTNT	2893
Dd	254	CHDPI-----NIQFTSGTSSPKATILSHINYNNSNIIERLKLHEKTEQOLRMILPNP	3088
Qy	290	IYIDLIGLGTLTPANKNGIAHLAKSSNFYAQLSQOFDAKE-----YRVLRCVD	3393
Dd	309	LYHCLGSVAGTMMCMWGATULLLASPIFNKGKALLEAISRGRTGYLPTPMFDILNQPD	3686
Qy	340	PANKEVEN-CAGVL 352	
Dd	369	FSSYDISTMCGAVI 382	

RESULT 15
US-09-989-722-194
Sequence 194, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deansoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavini, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C63
 CURRENT APPLICATION NUMBER: US/09/989,722
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 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match	5.4%;	Score 97;	DB 10;	Length 615;
Best Local Similarity	21.3%;	Pred. No. 2.3;		
Matches 54;	Conservative 50;	Mismatches 112;	Indels 38;	Gaps 10;

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Db	254	CHDPI-----NIQFTSGTSGPKGATLISHYNYVNNISMLIGRLKXHEKTPQLMILFNP	308
QY	290	LVIDLIGLGLTLPANKNGIAHLAKSSNFYQLSQOPAKESG-----VRVLEACVD	339
Db	309	LYHCLGSVAGTMMCLMGATLILASPFFNGKKALAEASRREGTFLYGTPTMFMDILNQPD	368
QY	340	PANKEVKN-CAGVL	352
Db	369	FSYSYDISTMCGVIL	382

Search completed: January 24, 2003, 19:43:54
Job time : 17 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 24, 2003, 19:40:55 ; Search time 17 Seconds
(without alignments)
616.151 Million cell updates/sec

Title: US-09-675-509-4
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Scoring table:

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Searched: 262574 seqs, 29422922 residues

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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	139.5	7.7	10182	US-09-134-001C-3159	Sequence 3159, Ap
2	103.5	5.7	397	US-09-134-001C-4104	Sequence 4104, Ap
3	98.5	5.5	1149	US-07-915-203-2	Sequence 2, Appl
4	98.5	5.5	1149	US-08-272-887-2	Sequence 2, Appl
5	98.5	5.5	1149	US-08-769-449-2	Sequence 2, Appl
6	97.5	5.4	624	US-09-336-447A-7	Sequence 7, Appl
7	97.5	5.4	639	US-09-134-001C-5661	Sequence 5661, Ap
8	97.5	5.4	825	US-09-540-824-26	Sequence 26, Appl
9	97.5	5.4	2037	US-09-306-998-3	Sequence 3, Appl
10	93	5.2	348	US-07-989-845-2	Sequence 2, Appl
11	93	5.2	348	PCT-US93-11298-2	Sequence 2, Appl
12	92.5	5.1	607	US-09-204-208A-11	Sequence 11, Appl
13	92.5	5.1	831	US-09-269-861A-8	Sequence 8, Appl
14	92.5	5.1	3418	US-08-639-501-2	Sequence 2, Appl
15	92.5	5.1	3418	US-08-603-753D-4	Sequence 4, Appl
16	92.5	5.1	3418	US-09-044-946-2	Sequence 2, Appl
17	92.5	5.1	3418	US-08-755-587-44	Sequence 44, Appl
18	92.5	5.1	3418	US-09-044-908-2	Sequence 2, Appl
19	92.5	5.1	3418	US-09-099-753-4	Sequence 4, Appl
20	92.5	5.1	3418	US-08-986-106-4	Sequence 4, Appl
21	92	5.1	468	US-08-961-083-10	Sequence 10, Appl
22	91.5	5.1	386	US-09-134-001C-3809	Sequence 3809, Ap
23	91.5	5.1	1211	US-09-134-001C-4820	Sequence 4820, Ap
24	91	5.0	279	US-09-134-001C-4222	Sequence 4222, Ap
25	91	5.0	1285	US-07-582-945-2	Sequence 2, Appl
26	91	5.0	1285	US-08-453-141-2	Sequence 2, Appl
27	91	5.0	1285	US-08-293-314-2	Sequence 2, Appl

28	90.5	5.0	707	4	US-09-134-001C-2362	Sequence 2362, Ap
29	90.5	5.0	2366	1	US-08-480-604A-10	Sequence 10, Appl
30	90.5	5.0	2366	2	US-08-405-496A-10	Sequence 10, Appl
31	90.5	5.0	2366	4	US-08-915-136-10	Sequence 10, Appl
32	90.5	5.0	2366	4	US-08-957-310-10	Sequence 10, Appl
33	90	5.0	384	1	US-08-220-958-2	Sequence 2, Appl
34	90	5.0	434	4	US-09-134-001C-4251	Sequence 4251, Ap
35	90	5.0	454	4	US-09-416-050A-6	Sequence 6, Appl
36	90	5.0	454	4	US-09-664-800-6	Sequence 6, Appl
37	90	5.0	454	4	US-09-665-309-6	Sequence 6, Appl
38	90	5.0	454	4	US-09-661-569-6	Sequence 6, Appl
39	90	5.0	1024	4	US-09-091-117-5	Sequence 5, Appl
40	89.5	5.0	1098	1	US-07-777-715-7	Sequence 7, Appl
41	89.5	5.0	1098	1	US-08-170-126-2	Sequence 2, Appl
42	89.5	5.0	1098	3	US-08-954-418-2	Sequence 2, Appl
43	89.5	5.0	2183	1	US-08-348-891A-7	Sequence 7, Appl
44	89.5	5.0	2183	2	US-08-905-817-7	Sequence 7, Appl
45	89	4.9	892	4	US-09-336-447A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
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; Sequence 3159, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/134, 001C
; PRIOR FILING DATE: 1998-08-13, 001C
; PRIOR APPLICATION NUMBER: US 60/064, 964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055, 779
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3159
; LENGTH: 10182
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3159

Query Match 7.7%; Score 139.5; DB 4; Length 10182;
Best Local Similarity 20.5%; Pred. No. 0.0095;
Matches 89; Conservative 59; Mismatches 140; Indels 147; Gaps 17;

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DB	8978	NNQAFPPQVQASNYNSDEDLKQCFDHALSNARKVLAKENGKNDLDEKOIOGKQVY-----	9032
QY	154	SSSFTVFGLYQ-----QLQS-----SSSAVDIKASD	182
DB	9033	EDTDALNGIORLSKAKAKAIQYQVSLSYINDAQRHIAENNINNSDLSTLANTLSKASD	9092
QY	183	LPOSGDVNNDITQKYRTITLSTVVASQREYINSVKGKPISNVYGVSSMCEIKDIIR	242
DB	9093	L---DNAMDLRPTIS--NSTSVPSNVYINADK-----NLQIEFDEAL-----	9132
QY	243	DQYNNVQIGTSKRPYYTVDVLANSNLCDK-----QYVAEVIYKLLTNLTVLVDLLG	296
DB	9133	-QQASATSSKTSSENPATIEEVLGLSQAIYDTKVALNGEQLATEKSKDLTKIKGLKDLNK	9191

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QY 297 LGTLTPANK-----NGIAHLKSSNFAQSLQCPDAESEVRU-----RCVDE-- 340
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QY 341 --ANKEVNKAGYL 352
Db 9252 KROFNKALKKAGYL 9266

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RESULT 2
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 Sequence 4104, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: CFC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 4104
 LENGTH: 397
 TYPE: PRT
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-4104

Query Match 5.7%; Score 103.5; DB 4; Length 397;
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Db 61 DSPYFELHSAIKVAVVDYRLKAKTRAITNRIKKYTFELANTVISOQFEPGASQSSYV 120
QY 137 ELAOKVGEQIVYDP---VASSSFTVFGLYOOLLQSSSA--AVDIKASDLPOSGD 189
Db 121 E---KKMIKAIKRTKTDVLVGRASFIN---LISKYAKAEIVTAMENMFADHPDQ 171
QY 190 VAKDITQKRYRI--LDSTVVASQGEY-----INSVQKRPIS--- 224
Db 172 YOKELIAAYRINKITITLTVADQOKYOSOLKTPYVYI PMVTEKRIAPAKRRIISAGRL 231
QY 225 NYUYGV---RSMCEIKDIRDOYNOVLGTSDPK-----VYTDVLA 265
Db 232 EYEKGIDLLLESIRLIGEDLRQLVYDHAIIYSSGSKTSLVDFINQYHNDLIIKIEPTOE 291
QY 266 LNSNLCEK-----QKVAVEVIKMLTTVLTLDLTG-IGLTLPAKNGIAHLAKSSN 316
Db 292 LNNKLAOSKIVVPSRNGFCMIIILEAMVQONIVYISREGNVGPSIINNONGNGLVNYEN 351
QY 317 FYAQLSQQFPAKESFVRLRCVDFPANKVKNQACAGVLPF 355
Db 352 -VSEIAKRIDLTTOHYNELDI-----IEKSKTLOQF 383

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RESULT:
US-07-915-203-2
Sequence 2, Application US/07915203
Patent No. 5359048
GENERAL INFORMATION:
APPLICANT: Ohba, Michio
APPLICANT: Iwahana, Hidenori
APPLICANT: Sato, Reichi
APPLICANT: Suzuki, No. 5359048ukazu

```

1 APPLICANT: Ogiwara, Katsutoshi
2 APPLICANT: Sakanaka, Kazunobu
3 APPLICANT: Hori, Hideaki
4 APPLICANT: Asano, Shouji
5 APPLICANT: Kawasugi, Tadaaki
6 TITLE OF INVENTION: No. 5359048e1 Microorganism and Insecticide
7 NUMBER OF SEQUENCES: 2
8 CORRESPONDENCE ADDRESS:
9 ADDRESS: David R. Saliwanchik
10 STREET: 2421 N.W. 41st Street, Suite A-1
11 CITY: Gainesville
12 STATE: FL
13 COUNTRY: US
14 ZIP: 32606
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patentin Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/07/915,203
22 FILING DATE: 19920723
23 CLASSIFICATION: 424
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Saliwanchik, David R.
26 REGISTRATION NUMBER: 31,794
27 REFERENCE/DOCKET NUMBER: M/K 301
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 904-375-8100
30 TELEFAX: 904-372-5800
31 INFORMATION FOR SEQ ID NO: 2:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 1149 amino acids
34 TYPE: AMINO ACID
35 TOPOLOGY: linear
36 MOLECULE TYPE: protein
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[illegible]

RESULT 4
US-08-272-887-2


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; Sequence 2, Application US/08272887
; Patent No. 5747450
; GENERAL INFORMATION:
; APPLICANT: Ohba, Michio
; APPLICANT: Iwahana, Hidenori
; APPLICANT: Sato, Reichi
; APPLICANT: Suzuki, No. 5747450ukazu
; APPLICANT: Ogiwara, Katsutoshi
; APPLICANT: Sakanaka, Kazunobu
; APPLICANT: Hori, Hidetaki
; APPLICANT: Asano, Shouji
; APPLICANT: Kawasugi, Tadaaki
; TITLE OF INVENTION: No. 5747450el Microorganism and Insecticide
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272.887
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/915,203
; FILING DATE: 23-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/K 301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-272-887-2

; Match 5.5%; Score 98.5; DB 1; Length 1149;
; Local Similarity 22.6%; Pred. No. 2.3;
; Matches 91; Conservative 58; Mismatches 126; Indels 127; Gaps 25;
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Db 998 IPGNNYTSFTE-----LITNRLOQAMNLYDLONAIPNGDFRNGLSNNMNTSDVN 1045
QY 316 -----NPFYAOLSQOPFAKESEVRVRCVDFANKE 344
Db 1046 VQOLSDTSVLVIPWNSQVSOFTVQPNRYLKVLT--ARKE 1085

RESULT 5
US-08-789-449-2
; Sequence 2, Application US/08789449
; Patent No. 5824878
; GENERAL INFORMATION:
; APPLICANT: Ohba, Michio
; APPLICANT: Iwahana, Hidenori
; APPLICANT: Sato, Reichi
; APPLICANT: Suzuki, No. 5824878ukazu
; APPLICANT: Ogiwara, Katsutoshi
; APPLICANT: Sakanaka, Kazunobu
; APPLICANT: Hori, Hidetaki
; APPLICANT: Asano, Shouji
; APPLICANT: Kawasugi, Tadaaki
; TITLE OF INVENTION: No. 5824878el Microorganism and Insecticide
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,449
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,887
; FILING DATE: 08-JUL-1994
; APPLICATION NUMBER: US 07/915,203
; FILING DATE: 23-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/K 301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-789-449-2

Query Match 5.5%; Score 98.5; DB 2; Length 1149;
Best Local Similarity 22.6%; Pred. No. 2.3;
Matches 91; Conservative 58; Mismatches 126; Indels 127; Gaps 25;
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Db 842 CGVDRCSEQDYVAMNLENNGENNMSSDASHFPHIDTGEIDLENNTGI-MWEPKIP 900
QY 153 ASSSFTVFGYQOOLQSSSSAAVDIKASDLPQSGDQVN-KDITQKRTILSDTVVASQ 210
Db 901 TTNGNATIGNL-EFVEEG-----PLSGETLEMNQOQEQODQMARKRAASE 946
QY 211 REYINSVKQKRPISNYVYGE---SMCEIKDIIIRDQYVNLIGTSDKPYVYTVTLV- 264
Db 947 KTYX-AAKQA-IDRLFADYODQKLSGVMSDILAQNL-VQSI-----PYVNDALPE 997
QY 265 --AANSNLCDEKQKVAIVITKLLNTL--VLDLGLGLTLPAN-KNGIAHLAKSS--- 315
Db 998 IPGNMYTSFTS-----LTNRLQQAAMNLYDLQNAIPNGDFRGLSNMNTSDVN 1045
QY 316 -----NFYAQSQOFPKSESEVRVRCVDFPANK 344
Db 1046 VQQLSDTSVLYIPMNSQVSGQFTVQPNRYVLRVT-ARKE 1085

US-09-336-447A-7
; Sequence 7, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPI AND USP2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/336.447A
; CURRENT FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 624
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-7

Query Match 5.4%; Score 97.5; DB 4; Length 624;
Best Local Similarity 25.4%; Pred. No. 1.1;
Matches 67; Conservative 47; Mismatches 89; Indels 61; Gaps 18;

QY 102 SSASVNGSVGFQYLCNLF--LSSPNGTQOASSLLELAQVYE-QIVY---PDVASS 155
Db 230 SRARVNG-----LTLKNFSGVSKADGTVSVGS-----QGKERQIVHVGAGQISDD 275
QY 156 SSFTVFG--LYQOOLQSSSSAAVDIKASDLPQSGDQVNKDITQKRTILSDTVVASOREY 213
Db 276 STDVANGQLY-----ALATRVADNQNQDIENQDNT-KDL-QKXVKGLDKEVGLSHD- 326
QY 214 INSVKQKRPISNYVYGESEMCERDIIIRDQYVNLIGTSDKPYVYTVTLVNLNSMLCDE 273
Db 327 IGSLLHD--DVADNQADIAKNRADIKEL--DKEMV-----LSRDIYSINDVDADN 372
QY 274 KQKVA-----VEVINKLLTNTLVLDLGLGLTLPAN-KNGIAHLAKSSNFYAQSQQDA 327
Db 373 QADIAKQADIKTEENVEEG--LDLSGRLLIDQKADIDINNINHI-----YELAQOQDO 424
QY 328 KESEVRVLRVDFPANK--VKRCA 349
Db 425 HSDIKTLAKASAAVTDRIAKKA 448

RESULT 7
US-09-134-001C-5661
; Sequence 5661, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5661
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5661

Query Match 5.4%; Score 97.5; DB 4; Length 639;
Best Local Similarity 22.5%; Pred. No. 1.1;
Matches 74; Conservative 59; Mismatches 115; Indels 81; Gaps 19;

QY 60 SLDPVFTSDSIFLPYVLSLGVKSLDESLVGVGTGDLHSFVSSASVNGSVGFQYLC 119
Db 277 SYVDVMTSPFI--YRKXNAFSLTWTVTVSALTVSILCFALSRST-----LTN 324
QY 120 NFLSSPN-----GTQOASSLLELAQV-----GYEQIYVPDVASSSFTVFGLY- 164
Db 325 EVLLSPHDVTLKQKQAN--ELAFKLNRRNIEHYNYKXEVYAKYKDLFSE-GVYR 380
QY 165 -QQLQSSSSAAVDIKASD-----LPQSGDQVNKD--YQKRTILSDT-----VVASOR 211
Db 381 PKEITVTSDKYIPVSTRKQOTDIIIPRS--LKDVYKTDKRTAVAGSKFRLKVSRLR 437
QY 212 EYIN-----SVKQKRP--ISNYVYGESEMCERDIIIRDQ---QYVNLIGTSDKPYV 259
Db 438 KGIKRVYFMGSDVDRGRPTLLN-----DEDYQKREIKREKNIVSQGFPLKXNDJPEL 492
QY 260 YTDVLAISNLCDEKQKVAIVITKLLNTLVLDLGLGLTLPAN-KNGIAHLAKSSNFYA 319
Db 493 EKLVSINEDI-ETRSBASEI--SLTGLILFVTSFLGITFLAAGCIYI----- 541
QY 320 QLSQFPKSESEVR--VLRVDFPANK 345
Db 542 ---KQIDETEDELNNTYTLRKLGFTHDM 567

RESULT 8
US-09-540-824-26
; Sequence 26, Application US/09540824
; Patent No. 6383753
; GENERAL INFORMATION:
; APPLICANT: Thiele, Dennis
; APPLICANT: Liu, Phillip
; TITLE OF INVENTION: No. 6383753el Yeast and Mammalian Regulators of Cell Prolifera
; FILE REFERENCE: UM-0426
; CURRENT APPLICATION NUMBER: US/09/540,824
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentn version 3.0
; SEQ ID NO 26
; LENGTH: 825
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-09-540-824-26

Query Match 5.4%; Score 97.5; DB 4; Length 825;
Best Local Similarity 19.7%; Pred. No. 1.7;
Matches 81; Conservative 65; Mismatches 130; Indels 135; Gaps 20;

QY 24 NEVKLINLIKDV-----LPTQVSGY-NIEYTEFDCYDASLQSLPVDVSTDSIFLPYVSL 78
Db 413 SHVEVQLLKGLDYKDYPTVVSIRITLHVHKLHPDNKSRLEN---PSV--ILLQHTLHL 466

QY 79 GGVKSLDESLVGVGTGDLHSFVSSASVNGSVYGFQYLCNFISSPNGTQOASSLLEL 138
Db 467 TROPIMSMELLEHLTEHLHSLAQO-----FPSALGISF-LSVVEGMRK-----RL 510
QY 139 AOKVGYQIYPPDVASSSFTVFGLYQOQLLOSSSSAAVDIK-----ASDLPQSGDVNK 192
Db 511 AKSVYFPEIKPEP-----SDLLFENLTSGIFPTSDKKHIVSPVMTMAESLSOSPADSLS 567
QY 193 DITOK-----YRTILDSTVVASOREVI-----NSVKOGKP 222
Db 568 DVCKKLYIALFLKFGOSYRHYREVITAVSQALYLPNFISTVPGTALPDSLKE--- 624
QY 223 ISNVYVSSSKEIKDIIRDQYVQLIGTSDKP---YVYTDVALNSNCDE-----K 274
Db 625 -----KONLFAIQDISLDEPQRLSLYELEELPTGLLOSSILFIRLNLIMAMIDYFK 676
QY 275 QKXAVEI-----KULLNTLVLDLIG----- 296
Db 677 EQAFIEIFVPMQYLSKELSLKRLSEKLSLTLQAVSDSIESAKANKRKLALQSHR 736

QY 297 -LGIT--LPANKGIAHLAKSSNFY-----AQY-----SQGFADKSEVRLR 336
Db 737 PLGITSQVPRFEGYS-LDKSSHIDPERAQLNKLRAQHRDAKKGAIRTLR 786
RESULT 9
US-09-998-3
; Sequence 3, Application US/09306998
; Patent No. 6291173
; GENERAL INFORMATION:
; APPLICANT: Bartel, Paul L.
; APPLICANT: Tavitgian, Sean V.
; TITLE OF INVENTION: MMSC2- An MMAC1 Interacting Protein
; FILE REFERENCE: MMSC2
; CURRENT APPLICATION NUMBER: US/09/306,998
; EARLIER FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 60/084,740
; EARLIER FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2037
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-306-998-3

Query Match 5.4%; Score 97.5; DB 4; Length 2037;
Best Local Similarity 21.4%; Pred. No. 7.2;
Matches 75; Conservative 48; Mismatches 147; Indels 81; Gaps 15;
QY 7 TLTVGLFPVLPSPNNENGVKLNILIKDVLPYQVSGVNIETEDCYSDASLQSPVFS 66
Db 778 TVVIGVAKPLPLSPEDC---VYSAKED-----SFLYPPHSC-EEAGLADKP-LFR 822
QY 67 TDSIFLPYVLSLGVKSLDESLVGVGTGDLHSFVSSASVNGSVYGFQYLCNFISSP 126
Db 823 ADLA-----LVGTNDADVLDS-----TFESPSPENDSITYSQAAILSHGSSCG 868
QY 127 NGTQOASSLLELAOKVGYEQIYPPDVASSSFTVFGLY-----QQLLOSSSSAAVDI 178
Db 869 DGNVYSSLPSPSPK-----DVYENSCDPLDLHMSLELELYTNLLQORDENTPSV 919
QY 179 KASDLPQSGDVN-----KQITQKRTILDSTVVASOREVINSVKOKPISNVYVGSSES 233
Db 920 DIMGPRASGTTINDYPPANAIEQYF--CENTVWTESHPSEV-----IS 963
QY 234 MCEIKDIIRDQYVQLIGTSDKPYYVYTDVALNSNLCDEKQKXAVEIKULLTNTLVLD 293
Db 964 SAEPLPVLPS-----AGKSEYLLQSSSLACNAE-CVWLQVNSKSEFER--TINIAGK 1014
QY 294 LGLGLTLPANKGIAHLAKSSNFYQOQLSQGFADKSEVRLRCVDFANKE 344
Db 1015 NSSLGMTVSNKDKGLGIVRSIIHGAIIS-----RDGRIAIGDCIILSINEE 1060

RESULT 10
US-07-989-845-2
; Sequence 2, Application US/07989845
; Patent No. 5304472
; GENERAL INFORMATION:
; APPLICANT: Baes, Steven
; APPLICANT: Swartz, James
; TITLE OF INVENTION: METHOD OF CONTROLLING POLYPEPTIDE
; TITLE OF INVENTION: PRODUCTION IN BACTERIAL CELLS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080-4990
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,845
; FILING DATE: 19921120
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haack, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 752
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-989-845-2

Query Match 5.2%; Score 93; DB 1; Length 348;
Best Local Similarity 23.5%; Pred. No. 1.2;
Matches 52; Conservative 42; Mismatches 79; Indels 48; Gaps 10;
QY 100 VSSASVNGSVYGFQYLCNFISSPNGTQOASSLLELAOKVGYEQIYPPDVASSSFT 159
Db 23 VFAEASLTGAGATFPAPYAKWA-----DYOK-----ETGNKKNYOGI-----GSS-- 64
QY 160 VFELYQQLLOSSSSAAVDIKASDLPQSGDVNNDITQKRTILDSTVVASOREVINS--- 216
Db 65 --GGVQIITANT-----VDGASDAPLSDEKLAQEGLFQFTYIGGVVLANIPGLSSEL 118
QY 217 VKQGRISNVYGY-----SESMCEIKDIIRDQYVQLIGTSD---KPYVYTDVALNS 268
Db 119 VLDGKTLGIVYLGKIKMDDEAIKLPGLPSQVIAVVRADGSGTSFVFTSYLA--- 175
QY 269 NLCEKQKXAVEIKULLTNTLVLDLGLGLTLPANKGIA 309
Db 176 -----KVNEMKNNVGTGSTVKNPDIIG---GKNDGIA 206
RESULT 11
PCT-US93-11298-2
; Sequence 2, Application PC/TUS9311298
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: METHOD OF CONTROLLING POLYPEPTIDE PRODUCTION IN

TITLE OF INVENTION: BACTERIA
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11298
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 752
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-11298-2

Query Match 5.2%; Score 93; DB 5; Length 348;

Best Local Similarity 23.5%; Pred. No. 1.2;

Matches 52; Conservative 42; Mismatches 79; Indels 48; Gaps 10;

QY 100 VSSASVNGSYGPPQYICSNFLSSPNGTQOASLLELAQKVGVEQIVYDVASSSFT 159
DB 23 VFAEASLIGACATPPAPYAKWA-----DTYQK-----ETGNKVNQGI-----GSS-- 64
QY 160 VFGLYQQLQSSSSAAVDIKASDLPQSGDQVVKDITOKYRTILDSVVASQREYINSV-- 216
DB 65 ---GGVKQITANT---VDFGASDAPLSDSEKLAQEGLPFPVIVIGSVLAVNIPGLKSEL 118
QY 217 VKQKPEISNYVGY-----SESMEIKDIIIRDQYNVOLIGTSD---KPYVYTVLALNS 268
DB 119 VLDEGTLDIDILGKIKMDDEIAIKLNGKLPQGNIAVVRADSGSGTSFVTSYLA--- 175
QY 269 NLDEKQYAAVEVINKLLTNTVLVDLGLGLTPANKKGIA 309
DB 176 -----KYNEEMKNVGVGTVKMPIGG--GKANDGIA 206

RESULT 12

US-09-204-208A-11

Sequence 11, Application US/09204208A

Patent No. 6399320

GENERAL INFORMATION:

APPLICANT: Markau, Ureula

APPLICANT: Ebenbichler, Christine

APPLICANT: Achhammer, Gunthar

APPLICANT: Ankenbauer, Waltraud

TITLE OF INVENTION: Modified DNA-Polymerase from Carboxydotherrnus hydrogenoformans at

FILE REFERENCE: 4765

CURRENT APPLICATION NUMBER: US/09/204,208A

PRIOR FILING DATE: 1998-12-01

PRIOR APPLICATION NUMBER: EP/97121151.1

PRIOR FILING DATE: 1997-12-02

NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 607
TYPE: PRT
ORGANISM: Carboxydotherrnus hydrogenoformans
US-09-204-208A-11

Query Match 5.1%; Score 92.5; DB 4; Length 607;

Best Local Similarity 19.5%; Pred. No. 3.1;

Matches 67; Conservative 52; Mismatches 110; Indels 115; Gaps 15;

QY 21 ENGENEKLINLIDVLPYQVSGNIEYTERDCYSDASL-----QSLPVDV-----FST 67
DB 237 ELDEQIE--ELIREI-----VVLAGEERNLNSPRLQGYLFEKGLPIYKTKTKGYST 287
QY 68 DS-----IFLPYVLSLQGVKSLDE-----SLVGVGTDLHSFVSSASVNGSV 110
DB 288 DAEVLEELLPFHETIGKILNYRQMLKSTYTDGLMPLINERTGKLTHTTNGTGLTGR- 346
QY 111 YGFPQYLCNFFLLSPNGTQOASLLELAQV-----GYEQIYPPDVASSSFTVFG 162
DB 347 -----LASSERNLNIPRIELGRKRMFIPSPGYDIYSAD----- 384
QY 163 LYQQL-LQSSSSAAVDIKASDLPQSGDQVVKDITOKYRTILDSVVASQREYINSV-- 218
DB 385 -YSQIEHLRLAHFSEBPKLLEAYQKGEDIRKTASEVFGVLEVPENMAHAKSVNFGI 443
QY 219 -----QKPEISNYVGY-----SESMEIKDIIIRDQYNVOLIGTSDK 256
DB 444 VYGISDFGLGRDLKIPREAVAGKIKYFANYPKRYEVLDSVTAHREKGVTTLLFGR--R 501
QY 257 PYV-----YTDVLAALNSLCEDEKQYAAVEVINKLLTN 288
DB 502 RYIPELSSKQRTVQGFGERFAMNTPL-----QGSAAIDIIKLAMIN 541

RESULT 13

US-09-269-861A-8

Sequence 8, Application US/09269861A

Patent No. 6468775

GENERAL INFORMATION:

APPLICANT: Ankenbauer, Waltraud

APPLICANT: Markau, Ureula

APPLICANT: Svetlichny, Vitaly

APPLICANT: Schmitz-Agheguian, Gudrun

APPLICANT: Reiser, Astrid

APPLICANT: Angerer, Bernhard

APPLICANT: Ebenbichler, Christine

APPLICANT: Laue, Frank

APPLICANT: Bonch-Osmolovskaya, Elizaveta

TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASE FROM CARBOXYDOTHERMUS HYDROGENOFORMAN

FILE REFERENCE: 4494

CURRENT APPLICATION NUMBER: US/09/269,861A

PRIOR FILING DATE: 1999-11-22

PRIOR APPLICATION NUMBER: PCT/EP97/05391

PRIOR FILING DATE: 1997-10-01

PRIOR APPLICATION NUMBER: EP/96115873.0

PRIOR FILING DATE: 1996-10-03

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.0

SEQ ID NO 8

LENGTH: 831

TYPE: PRT

ORGANISM: Carboxydotherrnus hydrogenoformans

US-09-269-861A-8

Query Match 5.1%; Score 92.5; DB 4; Length 831;

Best Local Similarity 19.5%; Pred. No. 5.1;

Matches 67; Conservative 52; Mismatches 110; Indels 115; Gaps 15;

QY 21 ENGENEKLINLIDVLPYQVSGNIEYTERDCYSDASL-----QSLPVDV-----FST 67
DB 237 ELDEQIE--ELIREI-----VVLAGEERNLNSPRLQGYLFEKGLPIYKTKTKGYST 287

Db 461 ELGEQIE-ELIREI-----YVLAGEEFNLSNPROGLVLEFKGLPVIKKTGTGYST 511
Qy 68 DSIFLPLYL-----VSLGTVKSLDE-----SLVGVGTGDLSPVSSASVNGSV 110
Db 512 DAEVLEELLFPHEIGICKIINRYOMLTKSTYDMLINERCKLMTTNGTTLGR- 570
Qy 111 YGFPQYLCNFFLSSPNGTQOASSLLELAQV-----GYEQIVYPDVASSSFTVFG 162
Db 571 -----LASSEPNLQNIPIRELBGRKLRKMFIPSGDYIVGAD----- 608
Qy 163 LYQOOL-QOSSSSAAVDIKASDLPOSGDQVKNKDTQKRTITLDSVVASQREYINSV- 218
Db 609 -YSQIELRLLAHSESEKLEAVQKGEDIRKTASEVFGVSLSEVTPDEMAHAKSVNFGI 667
Qy 219 -----OGKPISNYYVG-----SESMCEIKDIIIPDOQVNVOLIGTSK 256
Db 668 VGISDPRGLRDLKIPREVAQKTIKYNFANYPKRYELDELVRFAREKGYTTLFG- 725
Qy 257 PYV-----YTDVLALNSLCEKQKQKVAVEVIKMLLTN 288
Db 726 RYIPELSSKRTVQGFERTAMNTPL-----QGSADITIKLAMIN 765
RESULT 14
US-08-639-501-2
Sequence 2, Application US/08639501
Patent No. 5837492
GENERAL INFORMATION:
APPLICANT: Tavligian, Sean V.
APPLICANT: Kamb, Alexander
APPLICANT: Simard, Jacques
APPLICANT: Couch, Fergus
APPLICANT: Rommens, Johanna
APPLICANT: Weber, Barbara
TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1001
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 22204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,501
FILING DATE: 29-APR-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/585,391
FILING DATE: 11-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/576,559
FILING DATE: 21-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/575,359
FILING DATE: 20-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/573,779
FILING DATE: 18-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-116802-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 3418 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-639-501-2
Query Match 5.1%; Score 92.5; DB 2; Length 3418;
Best local similarity 21.7%; Pred. No. 49;
Matches 86; Conservative 55; Mismatches 152; Indels 103; Gaps 22;
Qy 22 NGNEVKILNLIKD-----VLPTQVSGYNIETED---CYSDASLOSIPDVSTDS 69
Db 270 SGNISFK-VNSCKDHIGKSMNVLEDEYETVVDTSSEDSFSLCFPSKCRTNLOKVRTSKT 328
Qy 70 ---IFLPLVLSLGVKSLDE-----SLVGV-----TGDLHS-----FVSS 103
Db 329 RKKIF-----HEAVADCEKSKQVKEKYSFVSEVENDTDPDLSNVAHQKPFSSGS 380
Qy 104 ASVNGSVYGFPOYL-C-SNFLSSPNGTQ-QASSLELA---QKVGEOIVYPDVASSSS 157
Db 381 DKISKEV--VPSLACEWSQTLTSLGNGAQWMEKIPLHISCDQNISKDLDTENKPKKD 438
Qy 158 FTVPGLYQOLLQSSSSAAVDIKASDLPOSGDQVKNKDTQKRTITLDSVVASQREYINSV 217
Db 439 F-----LTSNSLP--RISSLPKSEKPLNEETVANKRP--EROHLSHTDCLAV 484
Qy 218 KQG---KPISNYYVGSESMCEIKDIIIPDOQVNVOLIGTSKPYVYTDVLALNSNL--- 270
Db 485 KQAIISGTSVPASSFGQIKSIIPRIRESPK-ETPNASFGMTDPNFKKETEASBSGEI 543
Qy 271 --CDEKO-KVAVEYIKN-----LNTVTLVLDLGLGLTLPANKNGIAHLAKSNFY--- 318
Db 544 TVCSQKEDSLCPNLIDNGSPATTQNSVALKNAGLSTLKKTKNTKIYAIHETFFKKG 603
Qy 319 -----AQLSQFDASEVRLRCVDFANKE 344
Db 604 KIPKQKSELINCSAQFEANAFAP---LTFANAD 635
RESULT 15
US-08-603-753D-4
Sequence 4, Application US/08603753D
Patent No. 5891857
GENERAL INFORMATION:
APPLICANT: Holt, Jeffrey T.
APPLICANT: Jensen, Roy A.
APPLICANT: Page, David L.
APPLICANT: King, Mary-Clair
APPLICANT: Szabo, Csilla I.
APPLICANT: Jetton, Thomas L.
APPLICANT: Robinson-Benton, Cheryl L.
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arles A. Taylor, Jr.
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 KB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/603,753D
FILING DATE: 20 FEB 1996

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/373,799
FILING DATE: 17 JAN 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3418
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens sapiens
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
CELL TYPE: normal breast tissue
CELL LINE: HMEC
ORGANELLE: no
FEATURE:
NAME/KEY: BRCA2 protein
LOCATION: 1 to 3418; Genbank locus HSU43746
IDENTIFICATION METHOD:
OTHER INFORMATION: BRCA2 protein has a negative
OTHER INFORMATION: regulatory effect on growth of human mammary cells
PUBLICATION INFORMATION:
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer
TITLE: susceptibility gene BRCA2
JOURNAL: Nature
VOLUME: 379
PAGES: 789-792
DATE: 1995
RELEVANT RESIDUES IN SEQ ID NO: 4: granin box
RELEVANT RESIDUES IN SEQ ID NO: domain at amino acids 3334-3344

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      5.1%: Score 92.5; DB 2, Length 3418;
      Local Similarity 21.7%: Pred No. 49;
      Chex 86; Conservative 55; Mismatches 152; Indels 103; Gaps 22.

QY      22 NGNEVLTILNLD-----VLPTQVSGYNIETEFD-----CYSPLAQSLPDVFSTDS 69
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      270 SGNNSRK-VNSCDHIGKSNPNVLEDEVEYTVVDTSBEDSFSLCFKCRKKNQXRTSMT 328
QY      70 ---FLPYIVLSIGVKSLE-----SLYRGV-----TGDLHS-----FVSSS 103
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      329 RKKIF-----HEANADECESKNQVKEKYSFVSEVEPNPTDPLDSNVAHQKPFSSS 380
QY      104 ASVNGSVYGFPOYLC-SNPLFSSPNRGT-QASSLLELA---QKYGEOIVYPDVASSSS 157
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      381 DKISKEV-VPLACWMSQTLTSLGNGAMEKRIPLHISSCQNISEKDLTDENTENRKKD 438
QY      158 FTFVGLYQQLLOSSSSAANDIKASDLPQSGDQVNDKITQKTIIDSTVVAQREYINV 217
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      439 F-----LISENSLP---RISLSPKSEKPLENETVANKKD--EEQHLSEHTDCLIAV 484
QY      218 KQG---KPISNVYVYGSSEMCETKIIINDQGVNQVLIGTSDKPYTYTIVLAINSL--- 270
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      485 KQAIQSTFSVASSFOQIKKISFPIRESPK-ETFNASFSGHMTDPNFKKTEASEGLETH 543
QY      271 --CDEKO-KVAEVIYN-----LNTNTLVLLDGLGLTPANKNGIAHLAKSSNPF--- 318
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

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Db      544  TVCQKQKESLCPNIDNGSWPATTTOGSAVLKXNAGLSLTKKTKNKRIYAIHDETFFYKGK 6033
QY      319  -----AQLSQQFDAKESEVRVLRCDVPANKE 344
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Db      604  KIPKDAQSELINGSAQGFANNFAP---LTFANAD 635

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Search completed: January 24, 2003, 19:43:37
Job time : 25 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2003, 19:37:09 ; Search time 38 Seconds

(Without alignments)
1248.348 Million cell updates/sec

Title: US-09-675-509-4

Perfect score: 1802
Sequence: 1 MSTOPKTLTVGLFPYLPSPWN.....CVDPAKKEVNCAGVLRPL 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139.5	7.7	10182	23	ABP38314
2	138.5	7.7	5024	22	AA682935
3	105.5	5.9	511	9	AA61161
4	104.5	5.8	511	9	AA61180
5	104.5	5.8	512	11	AA607574
6	104	5.8	753	23	ABP29819
7	104	5.8	751	23	ABP27624
8	103.5	5.7	397	23	ABP39259
9	103.5	5.7	4643	22	ABP71609
10	103	5.7	286	23	ABP53627

11	101.5	5.6	747	23	ABB90996
12	101.5	5.6	859	22	ABB71182
13	101.5	5.6	1787	23	ABB4791
14	101	5.6	346	15	AA60654
15	100.5	5.6	745	19	AAW73024
16	100.5	5.6	745	19	AAW78362
17	100	5.5	856	23	AA60651
18	99.5	5.5	889	23	ABB90898
19	99	5.5	1149	14	AA62354
20	98.5	5.5	1149	15	AA65162
21	98.5	5.5	1161	23	ABB5312
22	98.5	5.5	1239	20	AAV04734
23	98.5	5.5	1373	20	AAV04730
24	98.5	5.5	2000	20	AAV04732
25	98.5	5.5	2053	22	ABB7118
26	98.5	5.4	408	21	AA635740
27	98	5.4	456	21	AA635739
28	98	5.4	474	21	AA635738
29	98	5.4	624	19	AA68204
30	97.5	5.4	639	23	ABP40816
31	97.5	5.4	2037	21	AAV53753
32	97.5	5.4	2070	20	AAV04733
33	97.5	5.4	2701	17	AA69850
34	97.5	5.4	461	23	AA664816
35	97	5.4	461	23	AAV96176
36	97	5.4	487	22	AA681291
37	97	5.4	615	21	AA624068
38	97	5.4	615	21	AAV6678
39	97	5.4	615	22	AA665201
40	97	5.4	644	22	AA670158
41	97	5.4	1075	22	AA630804
42	97	5.4	470	21	AAV79305
43	96.5	5.4	2662	23	ABB91373
44	96.5	5.3	637	23	ABB49873
45	96				

ALIGNMENTS

RESULT 1
ABP38314 standard; Protein; 10182 AA.
XX
AC ABP38314;
XX
DT 24-UTL-2002 (first entry)
XX
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3159.
XX
KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KW antibacterial; gene therapy.
XX
OS Staphylococcus epidermidis.
XX
PN US6380370-B1.
XX
PD 30-APR-2002.
XX
PF 13-AUG-1998; 98US-0134001.
XX
PR 14-AUG-1997; 97US-055779P.
XX
PR 08-NOV-1997; 97US-064964P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Doucette-Stamm LA, Bush D;
XX
DR WPI; 2002-381255/41.
XX
DR N-PSDB; ABN90859.
XX
PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections -

Herbicidally activ
Drosophila melanog
Lactococcus lactis
p6ts variant. Bac
Helicobacter pylori
H. pylori bacteria
p6ts variant. Bac
Herbicidally activ
Herbicidally activ
Coleoptera toxin f
B.thuringiensis se
Lactococcus lactis
protein containing
protein containing
Protein containing
Drosophila melanog
Zea mays protein f
Zea mays protein f
Zea mays protein f
M. catarrhalis str
Staphylococcus epi
Amino acid sequenc
Protein containing
Human type 3 insul
Human albumin fusi
Human AFP protein
Human PRO1009 prot
Membrane-bound pro
Human PRO1009 (UNQ
DNA encoding human
Amino acid sequenc
Plasmodium falcipa
Herbicidally activ
Listeria monocytog

XX Disclosure; SEQ ID 3159; 267bp; English.
PS
CC ABN90538 to ABN93374 represent *Staphylococcus epidermidis* open reading
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC given in ABP35124 to ABP37960. The *S. epidermidis* sequences have
CC antibacterial activity and can be used in gene therapy. The sequences
CC can also be used in the diagnosis and treatment of bacterial infections,
CC particularly *S. epidermidis* infections. The sequences can be used to
CC screen for compounds able to interfere with the *S. epidermidis* life
CC cycle or inhibit *S. epidermidis* infection.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC USPTO web site.
XX
SQ Sequence 10182 AA;
Query Match 7.7%; Score 139.5; DB 23; Length 10182;
Best Local Similarity 20.5%; Pred. No. 0.17;
Matches 89; Conservative 59; Mismatches 140; Indels 147; Gaps 17;
QY 24 NEVKILMLKDVLPYQVSGVNIETFPDCYSDASLQSLPVFSTDSIFLPYVSLGVKS 83
DB 8873 NFTAQINNADAL-NKTOGQNLDFNADTFKD-----DIFKTKD-----ALNGIER 8917
QY 84 L-----DESLVRGVTDGLHSFVSSASVNGSV----- 110
DB 8918 LTAASKAERKLIIDSLKFINKAQFTHANDEIMNTNSIAQLSRIVQAQFDLNDAMKSLDEL 8977
QY 111 --YGFPOYLCSNFFLSSPNGTQOASLLELAQV-----GYEQIVYPDVA 153
DB 8978 NNQAFPVQOASSNYINSDBDLKQDFDHALSNARKYLAKENGKNDKEKQIQGLKQYI----- 9032
QY 154 SSSSFTVFGLYQ-----QLIQS-----SSSAVDIRASD 182
DB 9033 EDTKDALNGIORLSKAKAKAIQYVOSLSYINDAQRHIAENNIHNSDDLSTANTLSKASD 9092
QY 183 LPQGGDVNKKDITQKYRTILDSTVVASOREYINSVKQKPISNYYVGSEMCETKIDIR 242
DB 9093 L-----DNAMKDLRDTLES--NSTSVPSNVYINADK-----NLOIEFDEAL----- 9132
QY 243 DQGVNVQLIGSDKPYVYTVDLALNSNLCDEK-----QKVAVEVIKNLNTLVLDLLG 296
DB 9133 -QOASATSSKTSSENPAITEEVILGSAIYDTKMLNGEQRATEKSKDKLIKGLKDLNK 9191
QY 297 LGLTLPAK-----NGIAHLAKSNFYAQLSQQFPAKSEVRVL-----RCVDF-- 340
DB 9192 AQLIEDVTNKVNSANTLTLSLTOSTLTLELNDKMLLRDKLTLVNPVKASLNYRNADYNL 9251
QY 341 --ANKEVKNCAGYL 352
DB 9252 KRQFNKALKEAKGYL 9266
RESULT 2
AAG82935
ID AAG82935 standard; Protein; 5024 AA.
AC AAG82935;
XX
DT 03-SEP-2001 (first entry)
XX
DE *S. epidermidis* open reading frame protein sequence SEQ ID NO:2964.
XX
KM *Staphylococcus epidermidis* SRI strain; infection; diagnosis;
KM vaccination; endocarditis.
XX
OS *Staphylococcus epidermidis*.
XX
FN WO200134809-A2.
XX
PD 17-MAY-2001.
XX

PF 09-NOV-2000; 2000WO-US30782.
XX
XX 09-NOV-1999; 99US-0164258.
PR
XX (GLAXO) GLAXO GROUP LTD.
PA
XX
XX Kimerly Wu;
PI
XX WPI; 2001-316495/33.
DR N-PSDB; AAH53785.
PT
XX Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*,
PT useful for vaccinating against infections, e.g. endocarditis -
XX
XX Claim 18; Page 779-781; 2188bp; English.
PS
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG81454 to AAG83120, from *Staphylococcus epidermidis*.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC *S. epidermidis* polypeptides (II) via the production of vectors
CC containing them which are used to produce host cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of *S. epidermidis* infections, e.g. endocarditis. AAH5371 to
CC AAH55090 represent specifically claimed *S. epidermidis* genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
XX
SQ Sequence 5024 AA;
Query Match 7.7%; Score 138.5; DB 22; Length 5024;
Best Local Similarity 20.5%; Pred. No. 0.075;
Matches 89; Conservative 59; Mismatches 140; Indels 147; Gaps 17;
QY 24 NEVKILMLKDVLPYQVSGVNIETFPDCYSDASLQSLPVFSTDSIFLPYVSLGVKS 83
DB 3927 NFTAQINNADAL-NKTOGQNLDFNADTFKD-----DIFKTKD-----ALNGIER 3971
QY 84 L-----DESLVRGVTDGLHSFVSSASVNGSV----- 110
DB 3972 LTAASKAERKLIIDSLKFINKAQFTHANDEIMNTNSIAQLSRIVQAQFDLNDAMKSLDEL 4031
QY 111 --YGFPOYLCSNFFLSSPNGTQOASLLELAQV-----GYEQIVYPDVA 153
DB 4032 NNQAFPVQOASSNYINSDBDLKQDFDHALSNARKYLAKENGKNDKEKQIQGLKQYI----- 4086
QY 154 SSSSFTVFGLYQ-----QLIQS-----SSSAVDIRASD 182
DB 4087 EDTKDALNGIORLSKAKAKAIQYVOSLSYINDAQRHIAESNIHNSDDLSTANTLSKASD 4146
QY 183 LPQGGDVNKKDITQKYRTILDSTVVASOREYINSVKQKPISNYYVGSEMCETKIDIR 242
DB 4147 L-----DNAMKDLRDTLES--NSTSVPSNVYINADK-----NLOIEFDEAL----- 4186
QY 243 DQGVNVQLIGSDKPYVYTVDLALNSNLCDEK-----QKVAVEVIKNLNTLVLDLLG 296
DB 4187 -QOASATSSKTSSENPAITEEVILGSAIYDTKMLNGEQRATEKSKDKLIKGLKDLNK 4245
QY 297 LGLTLPAK-----NGIAHLAKSNFYAQLSQQFPAKSEVRVL-----RCVDF-- 340
DB 4246 AQLIEDVTNKVNSANTLTLSLTOSTLTLELNDKMLLRDKLTLVNPVKASLNYRNADYNL 4305
QY 341 --ANKEVKNCAGYL 352

Db 4306 KROENKALKEAKGV 4320

RESULT 3

AAP81161

ID AAP81161 standard; protein; 511 AA.

AC AAP81161;

DT 12-OCT-1990 (first entry)

DE Recombinant alpha-amylase.

KW Alpha amylase; yeast; brewing; baking.

OS Schwanniomycetes castellii ATCC 26076.

PN EP257115-A.

PD 02-MAR-1988.

PF 21-AUG-1986; 86EP-0111586.

PX 21-AUG-1986; 86EP-0111586.

PA (HETB) HEINEKEN TECHNISCH BEHEER BV.

PI Straesser A, Martens FB, Dohmen J, Hollenberg CP;

DR WPI: 1988-057532/09.

DR N-PSDB; AAN81477.

PT Prodn. of amylolytic enzymes by transformed microorganisms -
 PT comprises use of recombinant DNA technology to give transformant
 PT having DNA from donor yeast.

PS Disclosure; P; English.

CC The sequence encoding the protein can be used to construct an
 CC expression vector for the prodn. of alpha amylase in yeast cells.
 CC The transformants and recombinant enzyme produced can be used in
 CC fermentation processes e.g in baking and brewing. The transform
 CC yeasts are esp. suitable for prodn. of low carbohydrate beers.

SQ Sequence 511 AA;

Query Match 5.9%; Score 105.5; DB 9; Length 511;
 Best Local Similarity 22.0%; Pred. No. 1.9;

Matches 80; Conservative 48; Mismatches 117; Indels 119; Gaps 21;

```

QY 18 SMNENGENEYKLIILKDVLPQTQ-----VSGYNIETFEPCYSDASLOSLEDPVFSF 67
DB 159 AMNGDSSVD---YSSFTPFNOQSYFHDYCLITYNNDQTNVEDCWEQDTEVSLPDLSTE 214
QY 68 DS-----IFLPYLVSLGVKSLD-----ESLVRGVTGDLHSFVSSASVN-GSVY-GFPQYL 117
DB 215 DNEVIGVFOPTWSDPVQVNSIDGLRIDSAKHVDTSLTKEFEDASGVYNGEYQGDPTTY 274
QY 118 C-----SNFLSSP-----NGTQASSLLELAQKV-----GYE 145
DB 275 CPYQNYMKGVNTNPLYYPVYRPFSDTSATSS--ELTSMISTLOSQSCDVSLGNFIENHD 332
QY 146 QIVYPDVASSSS-----FTVFG-----LY-----QQLLOSSSSAA-----VDIK 179
DB 333 QVRFPSVTSVDTSLIKDMAFIIIGDGIPIITYGQGLNGSGDPANREALWLSGYNTDSE 392
QY 180 ASDLPQSGQVNDITQK---YRTILDSTVVASQREYINSVK-----218
DB 393 YYELISKLQNIQIRQAIKDSAVST-YKSSVSSSDHYIATRKSQDANQILSIFNNLSNG 451
QY 219 -QCKPISNRYVYGSESMCEIKDIR-----DQYNNQOLISTSKPYVYTDVLANSN 269
DB 452 GQDITVSN--TGYS--SGDKVIDIISCNVLAGSGLSVSISSGRMPQVYAPSSVLS--GSG 507

```

QY 270 LCDE 273

Db 508 ICNQ 511

RESULT 4

AAP81180

ID AAP81180 standard; protein; 511 AA.

AC AAP81180;

DT 12-DEC-1990 (first entry)

DE Sequence of alpha-amylase encoded by genomic DNA of Schwanniomycetes
 DE castellii.

KW Brewing; beer; breadmaking; bioass.

OS Schwanniomycetes castellii.

PN EP260404-A.

PD 23-MAR-1988.

PF 17-JUL-1987; 87EP-0110370.

PX 17-JUL-1987; 87EP-0110370.

PA (HETB) HEINEKEN TEC BEHEER NV.

PI Straesser A, Martens FB, Dohmen J, Hollenberg CP;

DR WPI: 1988-078794/12.

DR N-PSDB; AAN81525.

PT Polypeptide prodn. from cells transformed with yeast DNA -
 PT esp. coding alpha amylase or glucosylase, able to convert
 PT starch to ethanol

PS Claim 18; Fig 2A-2C; 74pp; English.

CC A cosmid library is constructed from genomic DNA of ATCC26076 and this
 CC screened for inserts contg. the Aa gene by ability to transform
 CC S.cerevisiae GRF 18 to histidine prototrophy. One positive cosmid
 CC (32kb; pYcl) was digested with EcoRI, religated and used to transform
 CC E.coli JAZ21. Positive transformants contain pYcl-alpha, which includes
 CC a 5kb EcoRI fragment contg. the gene in AAN81525.

SQ Sequence 511 AA;

Query Match 5.8%; Score 104.5; DB 9; Length 511;
 Best Local Similarity 22.7%; Pred. No. 2.3;

Matches 83; Conservative 44; Mismatches 116; Indels 123; Gaps 22;

```

QY 18 SMNENGENEYKLIILKDVLPQTQ-----VSGYNIETFEPCYSDASLOSLEDPVFSF 67
DB 159 AMNGDSSVD---YSSFTPFNOQSYFHDYCLITYNNDQTNVEDCWEQDTEVSLPDLSTE 214
QY 68 DS-----IFLPYLVSLGVKSLD-----ESLVRGVTGDLHSFVSSASVN-GSVY-GFPQYL 117
DB 215 DNEVIGVFOPTWSDPVQVNSIDGLRIDSAKHVDTSLTKEFEDASGVYNGEYQGDPTTY 274
QY 118 C-----SNFLSSP-----NGTQASSLLELAQKV-----GYE 145
DB 275 CPYQNYMKGVNTNPLYYPVYRPFSDTSATSS--ELTSMISTLOSQSCDVSLGNFIENHD 332
QY 146 QIVYPDVASSSS-----FTVFG-----LY-----QQLLOSSSSAA-----VDIK 179
DB 333 QVRFPSVTSVDTSLIKDMAFIIIGDGIPIITYGQGLNGSGDPANREALWLSGYNTDSE 392
QY 180 ASDLPQSGQVNDITQK---YRTILDSTVVASQREYINSVK-----218
DB 393 YYELISKLQNIQIRQAIKDSAVST-YKSSVSSSDHYIATRKSQDANQILSIFNNLSNG 451
QY 219 -QCKPISNRYVYGSESMCEIKDIR-----DQYNNQOLISTSKPYVYTDVLANSN 269
DB 452 GQDITVSN--TGYS--SGDKVIDIISCNVLAGSGLSVSISSGRMPQVYAPSSVLS--GSG 507

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D	b		393	YVELISKUNQIRNOAIKDSAYST-YKSSVSSSDHYIATRKGSDAQAOLISFNNGSNG	451
O	y		219	-QGKRISNYVGYSSEMCIEKDIIIPDOQYNVOLIGTSDK-----PYVTDTVALN-	267
			: : : : :	: : : : :	: :
D	b		432	SODITVSN--TGYS-SGDKVADII---SCNSVLNAGSGSLSVISGMPQPVYAPASSVLSA	505
O	y		268	SNLCDE 273	
			: :		
D	b		506	SGICNQ 511	
R	E	S	RESULT 5		
A	R	O	AA007574		
I	D		AA007574 standard; protein, 512 AA.		
X	X				
A	C		AA007574;		
X	X				
D	T		02-FEB-1991 (first entry)		
X	X				
D	b		Alpha-amylase encoded by the AMY1 gene.		
K	M		Schwanniomycex yeast cells; expression cassette; alpha-amylase;		
K	M		marker gene; regulon; signal peptide; terminator;		
K	M		autonomously replicating sequence.		
X	X				
O	S		Schwanniomycex occidentalis.		
F	H				
F	H		Key location/Qualifiers		
F	T		Disulfide-bond 66..74 /note="1"		
F	T		Disulfide-bond 186..200 /note="2"		
F	T		Disulfide-bond 276..319 /note="3"		
F	T		Disulfide-bond 475..510 /note="4"		
X	X				
P	N		EPJ94538-A.		
X	X				
P	D		31-OCT-1990.		
X	X				
P	F		28-APR-1989; 89EP-0107780.		
X	X				
P	R		28-APR-1989; 89EP-0107780.		
X	X				
P	A		(RHEI) RHEIN BIOTECH GFS.		
X	X				
P	F		Hollenberg C, Strasser A;		
X	X		WPI; 1990-328670/44.		
D	R		N-PSDB; AA006388.		
P	T		Transformed Schwanniomycex yeast cells - contg. an expression		
P	T		cassette contg. regulon, DNA coding for foreign protein and		
X	X		terminator		
P	S		Disclosure; Fig 1B(1-6); 59pp; English.		
X	X				
C	C		The expression cassette may contain a regulon (R), a signal peptide		
C	C		sequence (S), a foreign protein sequence (F) and a terminator (T)		
C	C		of which R and/or S and/or T are derived from the alpha-amylase gene		
C	C		of S. occidentalis.		
C	C		R is pref. a 1.8 kb BglII-XhoI fragment (bases -1 to -540 of this		
C	C		sequence).		
C	C		S contains all or part of one of the sequences represented		
C	C		in AA006383-87.		
C	C		F is e.g. a cellulase, interleukin, insulin-like-growth factor,		
C	C		interferon etc.		
C	C		T is pref. all or part of the terminator of this sequence		
C	C		(bp 1537-1740).		
C	C		AMY1 acts as selective marker for the vector carrying the expression		
C	C		cassette.		
C	C		See also AA006389.		

XX	Sequence	512 AA;	5.8%;	Score 104.5;	DB 11;	Length 512;
XX	Query Match		22.0%;	Pred. No. 2.3;	Indels 119;	Gaps 21
XX	Best Local Similarity		48;	Mismatches 117;		
XX	Matches					
QY	18	SWNENGENEYKILINLKDVLPPTQ-----VSGYNIEYTEFDCYSASLQSLPDPVFS	67			
DB	160	ANNGGSSVD-----YSSFTFPNQOSYFHDYCLITYNNDGTNVEDCMEGDTEVSLPDLSTE	215			
QY	68	DS-----IFLPYLVSLGVKSLD-----ESLVRGVTDGLHSFVSSASVN-GSYV-GFPQYL	117			
DB	216	DNEVIGVFGPTWSDPEVQNSIDGLRIDSAKHVDTSALTRFEDASGVYXNGEYVQGDPTYT	275			
QY	118	C-----SNFLISSP-----NGTQASLLELAQKV-----GYE	145			
DB	276	CFYQWYMKGVNTPLYYPVYRFFSDTSATSS--ELTSMISTLQSGSDVSLGNFTENDH	333			
QY	146	QVYRDPVASSS-----FTVFG-----LY---QQLSSSSAA-----VDIK	179			
DB	334	QVRFPVSTSDTSLIKNDMAFILGDGIPITLYGQEGGLNGSDPANREALMLSGYNTDSE	353			
QY	180	ASDLPQSGQVKNMDITQK---YRTILDSTVVASQREYINSVK-----	218			
DB	394	YVELISKLNQIRNQAIKRSANST-YKSSVSSSDHYIATRKGSANDANQLISFNNGSNG	452			
QY	219	-QGKPISNYYVGYSESMECEIKDIIR-----DQYNNQLIGTSDKPYVYTDVYALNSN	269			
DB	453	SGDITVSN--TGYS-SGDKVIDIILCSNVLADGSGLSVSIISGMPQVYVAPSSVL-S-GSG	508			
QY	270	LCDE 273				
DB	509	ICNQ 512				
XX	RESULT 6					
XX	ABP29819					
XX	ID	ABP29819	standard;	Protein;	753 AA.	
XX	AC	ABP29819;				
XX	DT	02-JUL-2002	(first entry)			
XX	DE	Streptococcus polypeptide	SEQ ID NO 8814.			
XX	KW	Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;				
XX	KM	group A streptococcus; Streptococcus pyogenes; antibacterial;				
XX	KW	antiinflammatory; infection; vaccine; meningitis; gene therapy.				
XX	OS	Streptococcus agalactiae.				
XX	PN	MO200234771-A2.				
XX	PD	02-MAY-2002.				
XX	PF	29-OCT-2001; 2001WO-GB04789.				
XX	PR	27-OCT-2000; 2000GB-0026333.				
XX	PR	24-NOV-2000; 2000GB-0028727.				
XX	PR	07-MAR-2001; 2001GB-0005640.				
XX	PA	(CHIR-) CHIRON SPA.				
XX	PI	(GENO-) INST GENOMIC RES.				
XX	PI	Telford J, Maignani V, Margarit Ros YI, Grandi G, Fraser C,				
XX	PI	Tettein H;				
XX	DR	WPI; 2002-352536/38.				
XX	DR	N-PSDB; ABN70450.				
XX	PT	New Streptococcus protein for the treatment or prevention of infection				
XX	PT	or disease caused by Streptococcus bacteria, such as meningitis, and				

KM antibacterial; gene therapy.
 OS Staphylococcus epidermidis.
 FN US6380370-B1.
 PD 30-APR-2002.
 PF 13-AUG-1998; 98US-0134001.
 PR 14-AUG-1997; 97US-055779P.
 PR 08-NOV-1997; 97US-064964P.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PI Doucette-Stamm LA, Bush D;
 DR WPI; 2002-381255/41.
 DR N-PSDB; ABN91804.
 YY Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections -
 PS Disclosure; SEQ ID 4104; 267bp; English.
 CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have
 CC antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.
 CC N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
 SQ Sequence 397 AA;
 Query Match 5.7%; Score 103.5; DB 23; Length 397;
 Best Local Similarity 18.5%; Pred. No. 1.9;
 Matches 74; Conservative 72; Mismatches 142; Indels 111; Gaps 18;
 QY 52 CYSDDSLSLPDV---STDSEFLPYLVSLG-VKSLDE-----SLVNGV 92
 D 1 CYNDLINTENNEVFFAMKSFTEFMNITYAMGGTVKSVTLANTLAEKGPVTIISVFRGA 60
 QY 93 TG---DLHSFV-----SSASVANSVVGFPDYLCNFFLSSPNTQOASSLL 136
 D 61 DSPFEHLSAIVKVVVDYRLKLTNTRAITARIKYPFLNTKXVISOEPFKSGPSSIV 120
 QY 137 ELAQVQVEQIVYDP---VASSSFVFGLYQOQLQSSSSA---AVDIKASDLPOSGDQ 189
 D 121 E---KKMIKAIKHTKTVDLVGTRASFNI---LISKYAKAEIVTIAMEHNNPDAHPOQ 171
 QY 190 VNKDITQKYRIT--LDSTVVASQREY-----INSYKQCKPIS--- 224
 D 172 YQKEIIIAVFRNKNKLTITTLVADQOQYQSOQLKTPYVYIPNMVTEKRIAPAKNRITISAGRL 231
 QY 225 NYVVYGS---ESMCEIKDIIRDOQNVOLIGSDRP-----YYTTDVLA 265
 D 232 EYEKQYDILLBSIRLIQELRLQNLANTDVHLYSGSGKSTSLVDPTINOYHLNDLIKITYEPOE 291
 QY 266 LNSNLCDEK-----QKVAVEVIKNLLTNTLVLDLIG-LGLTLPANKNGIAHLAKSSN 316
 D 292 LNNKLAQSKIIVVPSRNEGFGMIILEAMQDNIIVISFEGNVGPDGSIINNGDGVLVNNEN 351
 QY 317 FYAQLSQQFDAKSESEVRVLRCDVPANKEVKNACAGVLRPP 355
 D 352 -VSELAKRIDLTTOHYNELDHI-----IENSKDTLKOP 383

ABB71609	standard; Protein: 4643 AA.
ID 7	ABB71609
XX	
AC	ABB71609;
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Drosophila melanogaster polypeptide SEQ ID NO 41619.
XX	
KW	Drosophila; developmental biology; cell signalling; insecticide;
KW	pharmaceutical.
XX	
OS	Drosophila melanogaster.
XX	
PN	WO200171042-A2.
XX	
PD	27-SEP-2001.
XX	
PF	23-MAR-2001; 2001WO-US09231.
XX	
PR	23-MAR-2000; 2000US-191637P.
PR	11-JUL-2000; 2000US-0614150.
XX	
PA	(PEKE) PE CORP NY.
XX	
PI	Venter JC, Adams M, Li FWD, Myers EW.
XX	
DR	WPI; 2001-656860/75.
DR	N-PSDB; ABL15712.
XX	
PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
XX	
PS	Disclosure; SEQ ID NO 41619; 21pp + Sequence Listing; English.
XX	
CC	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB16176-AB130511), expressed DNA sequences (AB101840-AB16175) and the encoded proteins (ABB57737-ABB72072).
CC	(ABB57737-ABB72072).
CC	The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
CC	
CC	
CC	
XX	
XX	
SO	Sequence 4643 AA;
Query Match	5.7%; Score 103.5; DB 22; Length 4643;
Best Local Similarity	20.9%; Pred. No. 70;
Matches 78; Conservative	50; Mismatches 110; Indels 135; Gaps 19;
Y	2 STOPKTLVGLFPYLPSPNENGNEVKLINLKDVLPQVSGN-----IEYTEFD- 51
Db	3531 NTTFPTFPI-----KSGNEGCLRLKDDSLRTPASFPNHLQDFYIQVAVFDNG 3580
Y	52 ---CYSDAISLQSLPDVFTSDSIFLPYLVSLGIVKSLDSLVRGVTDLHSPVS-----S 103
Db	3581 TTPLYSDA-----WVV-----VKIIESQVPIPTPLEVLTINSFDDPS 3619
Y	104 ASVNGSVYGPPO--YLGSNF-LLSPNGTQAASLLLEAQKVGEOIYF---DV----- 152
Db	3620 GAFIGKVAHSAQDKYDELNFSLVSGPDDMYQSKLFINSNTGK---IYALSNLDIGLYK 3676
Y	153 ---ASSSFTVFGLYQQLDSSSSAANDIKASDLPQSGDQVNNKDITKYRTILDSTVA 208
Db	3677 LNVSVSDKEFVFVSI-----VKINVELVTNDMLKESVIRFRISASEPL 3722
Y	209 SORF-YINSGVQGRPISNYVYGVSSEWCEIDIR-----DQ 244
Db	3723 SHRKTFMSIR-----NIMRQKQDVLITLQSDYQKASQAVGNRRARSDS 3770

QY 245 QYV-----OLIGTSDKPYVTDLALNSNLCDEKQVAVEIKMLTNTLVLDLGL 297
 DB 3771 DLNVFAVRKQOIIIPDSDEFPTSDEI---RQTLIDKQNEIENE-----TLVVEDV--L 3819
 QY 298 GLTLPANNGIAH 310
 DB 3820 PSTCOSMKNDCVH 3832

RESULT 10

ABB53627
 ID ABB53627 standard; Protein; 286 AA.

AC ABB53627;

DT 16-MAY-2002 (first entry)

DE Lactococcus lactis protein p1pD.

XX Bioynthesis; biodegradation; lactic bacterium; yogurt; cheese.

OS Lactococcus lactis IL1403.

PN FR2807446-A1.

PD 12-OCT-2001.

PF 11-APR-2000; 2000FR-0004630.

PR 11-APR-2000; 2000FR-0004630.

PA (INRG) INRA INST NAT RECH AGRONOMIQUE.

PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;

DR WPI; 2002-043418/06.

XX New nucleotide sequence useful in the identification of Lactococcus

XX lactic and related species -

XX Claim 6; SEQ ID NO 329; 2504bp; French.

CC The present invention is related to a Lactococcus lactis nucleotide

CC sequence (ABB90521) and related proteins (ABB53300-ABB55621). The

CC nucleic acid sequence is useful in the detection and/or amplification of

CC nucleic acid sequence, particularly to identify Lactococcus lactis or

CC related species. The proteins of the invention are useful for the

CC bioynthesis or biodegradation of a composition of interest. The

CC invention helps research in lactic bacteria, particularly useful in the

CC production of yogurt and cheese.

CC Note: The sequence data for this patent is based on equivalent patent

CC WO20017734 (published 18-OCT-2001) which is available in electronic

CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 286 AA;

Query Match 5.7%; Score 103; DB 23; Length 286;

Best Local Similarity 20.7%; Pred. No. 1.3;

Matches 44; Conservative 41; Mismatches 88; Indels 40; Gaps 8;

QY 13 PPVLPSPNNE--NGNEVKLINIKDVLPTQVSGYNIETFEPCYSASLQSLPDVFTDSI 70
 DB 99 YAYLSKSNKANKNGNIVS-----IGDTITPIHLSTKYKAVTEIPDKSTIALPNDVNESR 154
 QY 71 FLPLVLSIGVKSLSDESLVSGVTGDLHSFVSSASVNGSVGFPQYLCSNPLSSPNTQ 130
 DB 155 AL-YVLKNVAGLIKLDTS--RGALATVKDIRNP-----KGLIIEIDASQ 196
 QY 131 QASLLELAQKV--GEQIVVPDVASSSFTVFGLYQQLQSSSSAANDIKASDLDPQSDQ 189
 DB 197 TPRALDSVAALVINYVFAISAKISEKS-----IYQEPLENDASQMINFIANAOSDKNNK 251

QY 190 VNKDITQKRTILDSTVVASQREYINSVKQGP 222
 DB 252 VYKEVVKAY-----EOKNIADSIKKEYP 274

RESULT 11

ABB90996
 ID ABB90996 standard; Protein; 747 AA.

AC ABB90996;

DT 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NO 207.

XX Herbicidal; plant; agriculture; herbicide.

OS Arabidopsis thaliana.

PN WO200210210-A2.

PD 07-FEB-2002.

PF 28-AUG-2001; 2001WO-EP09892.

PR 28-AUG-2001; 2001WO-EP09892.

PA (FARB) BAYER AG.

PI Tietjen K, Weidler M;

DR WPI; 2002-269010/31.

XX Identifying plant target proteins for herbicidally active compounds,

PT comprising aligning and comparing nucleic acid or amino acid sequences

PT from plant with nucleic acid or amino acid sequences from non-plant

PT organisms -

XX Claim 5; SEQ ID NO 207; 261pp + Sequence Listing; English.

CC The invention relates to identifying target proteins

CC (ABB90790-ABB94016) for herbicidally active compounds, comprising

CC aligning and comparing nucleic acid or amino acid sequences from plant

CC with nucleic acid or amino acid sequences from non-plant organisms using

CC suitable search parameters, where plant sequences having an E-value

CC greater by a factor of 3 than the E-value of most similar non-plant

CC sequences are selected. The polypeptides or nucleic acids encoding them

CC are useful for identifying modulators. The identified modulators are

XX useful as herbicides.

XX Sequence 747 AA;

Query Match 5.6%; Score 101.5; DB 23; Length 747;

Best Local Similarity 25.9%; Pred. No. 7.2;

Matches 85; Conservative 48; Mismatches 110; Indels 85; Gaps 19;

QY 3 TOPKTLTVGLFPV--LPSMNN--GNEVKLINIKDVL---PTQVSGYNIETFEPCYSD 55
 DB 7 SQAFSLFLFLFLPLPSVSSQLSSSRTLLEIQKLVPPFLRSVN--WTNF-CYLP 63
 QY 56 AS-----LQSLPDVFTDSIPLPLVLSIGVKSLSDESLVR-GVT 93
 DB 64 SSPFKLTCNGHTVLTGNRTVKLPGRFSSSLF-TVLTLSNKT--SLVSGIS 120
 QY 94 GDLHSFV-----SSASVNGSVGFPQYLCSNPLSSPNTQOASLLELAQKVGEQIV- 148
 DB 121 GPLPSQIIRLSSSLQSN-----LSSNFI--SGNIPKEISSLKGLSLVLANNLFN 169
 QY 149 --YPDVASSSFTVFGLYQQLQSSSSAANDIKASDLPGSGDVNKKITQKRTILDSTV 206
 DB 170 GSVVDLRLGLNSLDELNGKNT--GREVVPSSLASN--TITSLKNSFGSK 216
 QY 207 VASQREYINSVKQGPISNYVG-----YSESMEIKIIRDOQVNLIGTSDKPYVYTD 262

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Db      217 IFEQIKKLNKLSLDSNKKFTGSGIPRFLSLPSLONLSLAQNL---LSGSLP----- 266
Qy      263 VLAINSNLCDEKQKVAVEVINKLITNTL 290
      267 ----NSSLCNSKLRILDVSRNLLTFEKL 269

RESULT 12
AB871182
ID      AB871182 standard; Protein; 859 AA.
XX      AC      AB871182;
XX      DT      26-MAR-2002 (first entry)
XX      DE      Drosophila melanogaster polypeptide SEQ ID NO 40338.
XX      KW      Drosophila; developmental biology; cell signalling; insecticide;
XX      KW      pharmaceutical.
XX      OS      Drosophila melanogaster.
XX      PN      WO200171042-A2.
XX      PD      27-SEP-2001.
XX      PF      23-MAR-2001; 2001WO-US092331.
XX      PR      23-MAR-2000; 2000US-191637P.
XX      PR      11-JUL-2000; 2000US-0614150.
XX      PA      (PEKE ) PE CORP NY.
PI      Venter JC, Adams M, Li PMD, Myers EW;
XX      DR      MPI: 2001-656860/75.
XX      DR      N-PSDB; ABL15285.
XX      PT      New isolated nucleic acid detection reagent for detecting 1000 or more
XX      PT      genes from Drosophila and for elucidating cell signalling and cell-cell
XX      PT      interactions -
XX      PS      Disclosure; SEQ ID NO 40338; 21np + Sequence Listing; English.
XX      CC      The invention relates to an isolated nucleic acid detection reagent
XX      CC      capable of detecting 1000 or more genes from Drosophila. The invention is
XX      CC      useful in developmental biology and in elucidating cell signalling and
XX      CC      cell-cell interactions in higher eukaryotes for the development of
XX      CC      insecticides, therapeutics and pharmaceutical drugs. The invention
XX      CC      discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX      CC      sequences (AB101840-ABL16175) and the encoded proteins
XX      CC      (AB857737-AB872072) .
XX      CC      The sequence data for this patent did not form part of the printed
XX      CC      specification, but was obtained in electronic format directly from WIPO
XX      CC      at ftp.wipo.int/pub/published_pct_sequences.
XX      SQ      Sequence 859 AA;

Query Match      5.6%; Score 101.5; DB 22; Length 859;
Best Local Similarity 22.5%; Pred. No. 8.9;
Matches 77; Conservative 46; Mismatches 150; Indels 69; Gaps 14

Qy      43 VNIETETPC-YSDASLQSLPDVFSTDSIFLPLVSLGCVKSLDSGLVNGVTGDLHSFVS 101
Db      256 YNNETVTFATGDEDESLQQQPSLRYRS--LRRTASTSPKSSKTKAKR---GKHPEPV 310

Qy      102 SSASVNGSYVGPQYICSNFLLSSPNGTQOASSLLELAKVGEQIVPVDVASSSSFYV 161
Db      311 ASWMSEQRVAGEPEVWC-----TLQKSIAGEAVK-NY-----TITSAVC 350

Qy      162 GYVQQLGSSSSAAVDIRKSDLPQSGDVNKK-----DITQKRTITLSDTVASQK-EVI 214

```

Db 351 KLVRLQOQALSLQVHFFERSERVLSGLQASSLPALAGATOLLSHLDDPTATLERGVFF 410

Qy 215 NSVKGKPIISNYVGVYSSEMCIEKIDIRDOQYNVOLIGTSPKYVYTDVLAINSNICDEK 274
411 NDAKIERR-----RYEQRLQJRTVSKOTRYSLE-----RQHYINLSELDVDQLKHH 459

Db 275 QKAVAEVIRKMLTNTLVLDL--LGGLTLPANKNGIAHLAK--SSNRYALSOOF----- 325
460 TLITRLRLFERLVRLVVISIEQSCDLLLRANINWATLMIDYDGFASLSDAFVONEAV 519

Qy 326 -----DAKSEVRVLR-----CYDPANKEKNCAGV 351
520 RTLLVVVDHKQSSVRALALRALATLTCAPQAINQUGSGCGI 561

Db

RESULT 13

ABBA9791

ID ABBA9791 standard; Protein; 1787 AA.

XX ABBA9791;

XX DT 05-FEB-2002 (first entry)

XX DE Listeria monocytogenes protein #2495.

XX AC Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;

XX DT vitamin B12; bacterial infection; disease.

KW Listeria monocytogenes.

XX OS

XX PN WO200177335-A2.

XX PD 18-OCT-2001.

XX PF 11-APR-2001; 2001WO-FR01118.

XX PR 11-APR-2000; 2000FR-0004629.

XX (INSP) INST PASTEUR.

PA Buchrieser C, Frangoul L, Couve E, Rueniok C, Fsihi H, Dehoux P;
PI Dusangret O, Chetouani F, Nedjari H, Glaser F, Kunst F, Coissart P;
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tietze-Martinez A, Amend A;
PI Charaborny T, Dommann E, Hahn T, Berche P, Chabdit A, Durant L;
PI Perez-Ijaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueno E, De Pablos B, Wehlund J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;

XX

XX DR WPI; 2002-010914/01.

XX

XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and
PT related polypeptides -

XX

PS Claim 6; SEQ ID No 2496; 192pp; French.

XX

XX The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see AB03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytogenes and related organisms,
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms.

CC Note: The sequence data for this patent did not form part of the printed

PT infections and gastroduodenal diseases
XX
PS Claim 9; Page 90-93; 184pp; English.
XX

CC This is the amino acid sequence of a 76 kDa Helicobacter pylori
CC polypeptide designated GHPO 1516. It was deduced from an isolated
CC genomic DNA sequence (see AAV07913). The invention provides a family
CC of 76 kDa Helicobacter polypeptides (see AAW73034), as well as a
CC 32 kDa polypeptide (see AAW73034) and a 50 kDa polypeptide (see
CC AAW73035), and also polynucleotides (see AAV72001, AAV07912-21 and
CC AAV07963-64) encoding them, expression cassettes, and methods for
CC producing the unprocessed or mature polypeptides in host cells. The
CC polypeptides can be used in vaccination methods to prevent or treat Hb
CC infection in a mammal. Methods and products of the invention allow
CC treatment and prevention of gastroduodenal diseases associated with Hb
CC infections, including acute, chronic, and atrophic gastritis, and
CC peptic ulcer diseases, e.g. gastric and duodenal ulcers. Detection
CC and diagnostic methods are also provided. GHPO 1516 was
CC demonstrated to be a protective antigen.

Sequence 745 AA;

Query Match 5.6%; Score 100.5; DB 19; Length 745;
Best Local Similarity 21.1%; Pred. No. 8.8;
Matches 63; Conservative 43; Mismatches 112; Indels 81; Gaps 11;

QY 103 SASVNGSVYGFPOYLCSNFLSPNG----- 128
DB 212 TADINGGVYQCK--AKNGSSSSSGNGSSQTATTGDDGVITTTYNKKATVKFDI 269
QY 129 TQASSLLELAKVGEIV---YPDVASSSFYVGLYQQLLOSSSAVDIKASDLPQ 185
DB 270 TNNAEQLNQANI--MVLNTQCPVSTNNENTPGGQPGWGLSTSGNACSI---FQQ 323
QY 186 SGGVKNKIDITQKVRTILSTVASOREYNSVKGKPISNYY-VGSESMCEIKDIIIRDQ 244
DB 324 EFSVTTSMIKNAQETIIAQSIVSENAQNNNDTGKFPNPTDASFAQSM-----LKNA 377
QY 245 QYNVOLIGTSDPKPYVYTVLALNSNLCDL-----KQYAVEVIKNL----- 286
DB 378 QAQAEMLPFLSEQVKNLEVMKNNNNVNEKLAGFGKEVMTNFSAFILASCKDGTLPNAG 437
QY 287 --TNTLVLDLGLGLTPANKGIIHLAKSSNFYAQLSQPDASEVRLRCVDFANK 343
DB 438 VTSNTWAGACAYGETTISALNTSIH-----FGTEQOIQAENIADTL--VNFKSR 487

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